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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | A48665 Sequence 3 | | | AA685004 Seguence | Segment | S | 90 | A48709 Sequence 47 | AX15/350 Sequence AX452796 Semience | AX685048 Sequence | A48711 Sequence 49 | AKIS/351 Sequence | AX685050 Sequence | AF207766 Hepatitis | AJ132996 Hepatitis | AF165056 Hepatitis | AF165055 Hepatitis | DS048S Heparitis C AB049101 Heparitis | E07544 Gene fragme | E09288 cDNA encodi | encodi | | E07391 cDNA encodi | AB008441 Hepatitis | AJ238800 Hepatitis D13558 Hepatitis C | D10934 Hepatitis C | AX739971 Sequence | AJ238799 Hepatitis | AXO36258 Sequence | AX036256 Sequence | AX036262 Sequence | D00689 Hepatitis C | AR027783 Sequence | Hepatiti | Hepati | Hepatiti | | | linear PAT 07-MAR-1997 | | | | | | Buyse, M. PROTEINS FOR DIAGNOSTIC AND | |
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| ID | - 99 | AR157324 | AX452752 | A48667 | AR157325 | AX452754 | AX685006 | A48709 | AX452796 | AX685048 | A48711 | AK15/351 AX452798 | AX685050 | AF207766 | HCV132996 | AF165056 | AF165055 | AB049101 | E07544 | E09288 | E04260 | E04805 | E07391 | | HCJ238800 HPCJ483 | HPCRNA | | | AA036252 | AX036260 | AX036262 | HPCPEP63 | AK027786 | AB008442 | AB008443 | нсуросур | ALIGNMENTS | | 642 bp | MO960M | | | | | ., De, VIRUS | 3 15-FEB-1996 |
| DB | ! | 9 | v v | ט ע | o w | 9 | 9 | ب و | 0 0 | 9 | · o | ص م | 9 | 4.4 | 14 | 14 | 14 | 1 4 | 9 | 9 7 | 9 | 9 | 9 | | 1 4 | 14 | 9 | 14 | ט ע | o vo | v | 14 | ی م | 14 | 14 | 14 | | | | aten | 02378 | | | 642) | 20 | 35-A |
| Length | 642 | 642 | 642 | 747 | 795 | 795 | 795 | 2082 | 2082 | 2082 | 2433 | 2433 | 2433 | 9379 | 9418 | 9386 | 9386 | 9598 | 3461 | 3461 | 2540 | 2540 | 2540 | 3296 | 9033 | 9456 | 9605 | 9605 | 11076 | 11076 | 11076 | 1054 | 1863 | 3296 | 3296 | 9379 | | | | 3 from Patent | GI:2302 | T G | e d | 1 to 64 | Maertens,G., Bosma. PURIFIED HEPATITIS | IC USE 0 9604385 |
| Query Match | 100.0 | 100.0 | 100.0 | | | | | | | | 96.5 | | | 89.6 | | ٠. | 88.3 | | 88.2 | | 88.1 | 88.1 | 88.1 | 88.1 | 88.T | 88.1 | 88.1 | 88.1 | 1.00 | 88.1 | | | 87.8 | | 87.8 | 87.8 | | | | | A48665.1 | dentif | unidentified | unciassified 1 (bases 1 | Maertens,G., PURIFIED HEP? | THERAPEUTIC USE Patent: WO 9604 |
| Score | 642 | 642 | 642 | 62B.2 | 628.2 | 628.2 | 628.2 | 619.8 | 619.8 | 619.8 | 619.8 | 619.8 | 619.8 | 575 | 569.6 | 568.6 | 567 | 567 | 566.4 | 566.4 | 565.4 | 565.4 | 565.4 | 565.4 | 565.4 | 565.4 | 565.4 | | 565.4 | | | | 563.8 | | | | | | | | | | | | | _ |
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Mismatches 0; Indels
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Other publication CA 2172273 960215
Other publication AU 382495 960304
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                                                                                   Maertens, G., Bosman, F., de Martynoff, G. and Buyse, M.A. Recombinant vectors for producing hov envelope proteins Patent: EP 1211315-A 3 05-JUN-2002; Innogenetics N.V. (BE)
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TTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIVMLLFAL"
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Purified Hepatitis C Virus envelope proteins for diagnostic threapeutic use
Patent: WO 0.2055548-A 3 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
therapeutic use 6245503-A 5 12-JUN-2001;
Patent: Us 6245503-A 5 12-JUN-2001;
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98.8%; Pred. No. 3.2e-147;
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Sequence 5 from patent US 6245503.
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AR157325.1 GI:16218258
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Best Local Similarity 98.8
Matches 633; Conservative
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QLLRRIPQAVVDMVAGAHWGVLAGIAYYSMVGNWAKVLIVMLLFAP"
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1 (bases 1 to 795)
Maertens, G., Bosman, F., De, M.G. and Buyse, M.
PURIPIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND
THERAPEUTIC USE.
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Pred. No. 3.2e-147;
0; Mismatches 8;
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/note="unnamed protein product"
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INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.
Location/Qualifiers
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Sequence 5 from Patent WO9604385.
A48667
A48667.1 GI:2302380
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Purified Hepatitis C Virus envelope proteins for diagnostic
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Patent: WO 02055548-A 5 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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Sequence 5 from Patent WO02055548.`
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/organism="Hepatitis C vi
/mol_type="genomic DNA"
/db_tref="taxon:11103"
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/db_zref="taxon:11103"
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INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.
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/note="unnamed protein product; Protein sequence is
conflict with the conceptual translation"

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IPRYRMYYGGVBHRFBAACMWTRGBRCDLBDRDRSBLSPLLLSTTBWOILPCSFTTLP
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AQABAALBNIVVLNAAAVAGAHGTLSFLVFFCAAWYIKGRLVPGAAYAFYGVWPLLLL
LLALPPRAYA"
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1 (bases 1 to 2082)

Maertens,G., Bosman,F., De Martynoff,G. and Buyse,M.-A.
Purified hepartis C virus envelope proteins for diagnostic and
therapeutic use
Patent: US 6245503-A 47 12-JUN-2001;
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Pred. No. 4.2e-145;
0; Mismatches 7;
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755 CTAAGGTTTTGGTTGTGTGTGTGCTACTCTTTGC 785
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Sequence 47 from patent
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AR157350.1 GI:16218284
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98.9%;
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Best Local Similarity 98.9
Matches 624; Conservative
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unidentified
unclassified.
1 (bases 1 to 2433)
1 (bases 1 to 2433)
1 (bases 2 to 2433)
1 (bases 2 to 2433)
Maertens, G., Bosman, F., De, M.G. and Buyse, M.
Maertens, G., Bosman, F. De, M.G. and Buyse, M.
THERAPEUTIC USE
PARENTIES OF 15-FEB-1996;
INNOGRNETICS NV (BE)
Other publication CA 2172273 960316.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    482 CAACGGCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG
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1. .2430
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Sequence 49 from Patent WO9604385.
A48711
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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purified Hepatitis C Virus envelope proteins for diagnostic and
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Pred. No. 4.2e-145;
0; Mismatches 7;
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Patent: WO 0205548-A 47 18-JUL-2002;
Patent: WO 0205548-A 47 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
1. .208="Hepatitis C virus"
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Sequence 47 from Patent WO02055548.
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Matches 624; Conservative
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VGDLCGSVFLVSQLFISPRRHETVQDCNCSIYVGHITCHRMADMMMWNSPTTTALVV
SQLLRIPQAVVDMYAGAHWGYLAGLAYYSMVGNWAKULVWLLFAGVDGHTRVSGGAA
SDTRGLVSLFSPGSAQKIQLVNTNGSWHINRTALNCNDSLQTGFFAALFYKHKENSS
GCPERLASCRSIBTRAQGWGPLTYTERNSSDQRPYCHTYARPROGTVPAGOVGCPYYC
FTDSPVVVGTTDRFCVPTYNWGANDDVLILNNTRPRCHWFGCTWMNGTGFTKTCGG
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TRYCKMYVGGVEHPFRAACMWTRGERCDLEDRDRSELSPLLLSTTEWQILDCSFTTL
PALSTGLIHLHQNIVUNAQAYGGAGVSLVIKWEYVLLIFFLLIADARICACLMMMLL
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PAT 17-OCT-2001

DNA

2433 bp US 6245503.

from patent

AR157351 Sequence 49 from patent AR157351 AR157351.1 GI:16218285

ACCESSION VERSION KEYWORDS

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1 (bases 1 to 2433)
Maertens,G., Bosman,F., De Martynoff,G. and Buyse,M.-A.
Purified hepatitis C virus envelope proteins for diagnostic
therapeutic use
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AX452798
AX452798.1 GI:21712483
                                                                 Patent: US 6245503-A
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| note="unnamed protein product" |
| codon start=1 |
| protein id="CAD38083.1" |
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| protein id="MSTNPKPQKKTRRNPERPRODVKFPGGGOIVGGVYLLPRRGPRL
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                            Maertens, G., Bosman, F., de Martynoff, G. and Buyse, M.A. Recombinant vectors for producing hcv envelope proteins Patent: EP 1211315-A 49 05-JUN-2002; Innogenetics N.V. (BE)
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/organism="Hepatitis C virus"
/mol_type="genomic DNA"
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                                                                                                                     Location/Qualifiers
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Qy 542 CGGGGGCCCATTGGGAATCCTGGGGGCTTCCACAAGCTGTGGGAACTGGT

Db 1046 CGGGGGCCCATTGGGAATCCTGGCGGCCTCGCCTACTATTCCATGGTGGGAACTGG 601

() 602 CTAAGGTTTTGATTGTGATGCTACTCTTTGC 632

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HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; huma: serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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                                                                                   ABK91411
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HCV B1 construct H
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HCV El construct H
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1 AIGCCCGGTIGCTCTTTCTC.....TACTCTTTGCTCTCTAATAG
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                    December 19, 2003, 16:53:58
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Listing first 45 summaries
                                                                     nucleic search, using sw model
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AAT12974
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642 642 628.2 628.2 619.8 619.8 619.8

Score

Result No.

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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1
and E2 protein coding sequence constructs. These sequences are included
in vectors for the production of recombinant E1, E2, and E1/E2 proteins.
The recombinant proteins can then be isolated using a method of the
constructs of the method, the envelope proteins are purified by
carrying out a disulphide bond cleavage, or a reduction step with a
carrying out a disulphide bond cleavage, or a reduction step with a
carrying out a disulphide bond cleavage, or a reduction step with a
carrying out a disulphide bond cleavage, or a reduction step with
CC flaulphide bond cleavage agent, after 1 psis of recombinant host cells.
The constructs containing the purified HCV envelope proteins can be used
The constructs can also be immobilised assay for detecting one or
antibodies in a sample, and in a serotyping assay for detecting one or
antibodies in a sample, and in a serotyping assay for detecting one or
constructs can also be immobilised on a solid substrate and incorporated
constructs can also be immobilised on a solid substrate and incorporated
constructs enversed phase hybridisation assay for determining the presence or
the genotype of HCV. The new purification method preserves the
conformation of the recombinantly expressed B1, E2 and B1/E2, and
conformation of the recombinantly expressed B1, E2 and B1/E2, and
conformation of more proteins. Antigens isolated using this method
conformation encouraminating proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 642; DB 17; Length 642; 100.0%; Pred. No. 1.3e-174; rive 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 642 BP; 109 A; 195 C; 176 G; 162 T; 0 other;
                                                                        Claim 23; Fig 21; 146pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     642; Conservative
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Best Local Similarity
                                           assays of HCV
                                                                                                                                                                                                                                                                                                                                                                                                          techniques.
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-epecific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligometric recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for transing nutrioning of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TGCGTTCGGGAGAACAACTCTTCCCGGTGCTTGGGTAGCGCTCACCCCCACGCTCGCAGCT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                               E2 protein; infection; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                      protein coding sequence.
GCTAAGGTTTTGATTGTGATGCTACTTTTGCTCTTAATAG 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 642; DB 24;
100.0%; Pred. No. 1.3e-174;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 158-159; 243pp; English.
                                                                                                                                                                                     Hepatitis C virus; HCV; El protein;
virucide; immunostimulant; vaccine;
                                                                                                                                                          E3
                                                                                                                                                                                                                                                                                                                                                                                                                Buyse M;
                                                                                                                                                          Hepatitis C virus clone HCCI9A
                                                                           BP.
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30-AUG-2001; 2001US-315768P.
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                                                                           DNA; 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-599657/64.
P-PSDB; AAO18660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from HCV infection
                                                                           AAL48913 standard;
                                                                                                                                                                                                                               Hepatitis C virus
                                                                                                                                                                                                                                                            WO200255548-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                   Maertens G,
                                                                                                                                    24-OCT-2002
                                                                                                                                                                                                                                                                                       18-JUL-2002.
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24-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                           HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) B1 and B2.protein coding sequence constructs. These sequences are included in vectors for the production of recombinant B1, E2, and B1/E2 proteins. The recombinant proteins can then be isolated using a method of the
                                                                                                                                                                           TATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCT
                                                                                                                                                                 ACAACGGCCCTGGTGTATCGCAGCTGCTCCCGGATCCCACAAGCTGTCGTGGACATGGTG
                                                           GCTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTGTCTTCCTCGTCTCC
                                                                            GCTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGGATCTGTCTTCCTCGTCTC
                                                                                           CAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATC
                                                                                                                               TATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
                                                                                                                                                                                                                                        642
                                                                                                                                                                                                                                                    GCTAAGGTTTTGATTGTGATGCTACTCTTTGCTCTCTAATAG
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                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                          E2; disulphide bond
                                                                                                                                                                                                                                                                                                    standard; DNA; 795
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                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus
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invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent. After 1918 of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed B1, E2 and B1, E2, and ellminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known
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97.9%; Score 628.2; DB 17
Best Local Similarity 98.8%; Pred. No. 1.3e-170;
Matches 633; Conservative 0; Mismatches 8;
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an E1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 206-209; 243pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition contenting at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an E1 and useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV sincipals or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                       New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                    E2 protein; infection; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch al Similarity 98.8%; Score 628.2; DB 24; Length 795; al Similarity 98.8%; Pred. No. 1.3e-170; 633; Conservative 0; Mismatches 8; Indels 0;
          Hepatitis C virus clone HCCI10A El protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 795 BP; 130 A; 240 C; 231 G; 194 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 161-162; 243pp; English.
                                     Hepatitis C virus; HCV; El protein; virucide; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                      Buyse M;
                                                                                                                                                                      11-JAN-2002; 2002WO-EP00219.
                                                                                                                                                                                                11-JAN-2001; 2001US-260699P.
                                                                                                                                                                                                                                           (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                        Bosman F,
                                                                                                                                                                                                                                                                                                   WPI; 2002-599657/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       from HCV infection
                                                                                  Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                  P-PSDB; AA018661.
                                                                                                               WO200255548-A2
                                                                                                                                                                                                                30-AUG-2001;
                                                                                                                                                                                                                                                                        Maertens G,
                                                                                                                                           18-JUL-2002
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                                                                                                                                                                                                                                                    CAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTG
                                                                                                                                                                                                                          CGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGG
                      ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA
                                                                                                                                                    CAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCAAAGCTGTCGTGGACATGGTGG
AGCTGTTCACCATCTCGCCTCGCCGCATGAGACGGTGCAGGACTGCAATTGCTCAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus E2 protein related coding sequence SEQ ID NO: 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E2 protein; infection; gene; ds.
                                                                                                                                                                                                                                                                                                          CTAAGGTTTTGATTGTGATGCTACTCTTTGCTCTCTAATAG 642
                                                                                                                                                                                                                                                                                                                                              CTAAGGTTTTGATTGTGATGCTACTCTTTGCTCCCTAATAG 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; El protein;
virucide; immunostimulant; vaccine;
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30-AUG-2001; 2001US-315768P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-599657/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus.
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94EP-0870132.

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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant El, E2, and El/E2 proteins. The recombinant proteins and the soldated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in viro detection on F HCV antibodies in a sample, and in a secrotyping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed El, E2 and El/E2, and eliminates contaminating proteins. Antigens isolated using this method elements are active with human sera than those isolated by known
                                                                                                                                                                                    Purifying recombinant hepatitis. C virus (HCV) El and E2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
                                                                                                                                                                                                                                                                                                          Claim 23; Fig 21; 146pp; English.
                                                (INNO-) INNOGENETICS
                                                                                            Bosman F, Buyse M,
                                                                                                                                           WPI; 1996-129401/13
    29-JUL-1994;
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                                                                                            Gaps
                                           DB 24; Length 2082;
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                                                                                            7; Indels
BP; 366 A; 634 C; 600 G; 482 T; 0 other;
                                         Score 619.8; DB 24
Pred. No. 4.9e-168;
0; Mismatches 7;
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                                           Match 96.5%;
Local Similarity 98.9%;
es 624; Conservative
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                                                                                                                                   17; Length 2086;
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0
                                                                                                                                                                                                                                                         Indels
Sequence 2086 BP; 366 A; 635 C; 601 G; 484 T; 0 other;
                                                                                                                      tch 96.5%; Score 619.8; DB 17; al Similarity 98.9%; Pred. No. 4.9e-168; 624; Conservative 0; Mismatches 7;
                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455
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95WO-EP03031

31-JUL-1995;

15-FEB-1996

Hepatitis C virus

WO9604385-A2

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us-09-899-303a-3.rng

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AAL48940
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                              694
                                                                                601
                                                                                                                                  754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                                             Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of di:eulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2433 BP; 434 A; 745 C; 714 G; 540 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus.
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96.5%; Score 619.8; DB 17; Length 2433; 98.9%; Pred. No. 5.2e-168; ive 0; Mismatches 7; Indels 0;

96.5 Best Local Similarity 98.9 Matches 624; Conservative

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                                                                                                                                                     GGAACGCCAGGGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGG
                                                                                                                                                                       746 dgaacdccadcdccaccaccacaacaaracdacdccacacarrrgcrcdrrddddd
                                                                                                                                                                                           CTGCTCTCTTTCCGCTATGTACGTGGGGGATCTGCGGGATCTGTCTTCCTCGTCTCCC
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                                                                                                                           GGTTCGGGAGAAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCGGGTAG
                                                                          Hepatitis C virus E2 protein related coding sequence SEQ ID NO: 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus; HCV; B1 protein; B2 protein; infection; gene; virucide; immunostimulant; vaccine; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL48940 standard; DNA; 2434 BP.
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30-AUG-2001; 2001US-315768P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-2002 (first entry)
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AAQ64068;
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                                                                                                                         The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition contenting at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV El and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                              purified
                                                                                                                                                                                                                                                                                                                                        Gaps
                                             New therapeutic vaccine compositions comprising at least one purifit recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
                                                                                                                                                                                                                                                                                                              94.8%; Score 608.8; DB 24; Length 2434; 98.7%; Pred. No. 7.6e-165; ive 0; Mismatches 7; Indels 1;
                                                                                                                                                                                                                                                                                       Seguence 2434 BP; 434 A; 745 C; 714 G; 541 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  632
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                                                                                                      Example 2; Page 212-215; 243pp; English.
                                                                                                                                                                                                                                                                                                                                       Matches 624; Conservative
            2002-599657/64
                                                                                 from HCV infection
                                                                                                                                                                                                                                                                                                                            Similarity
                       P-PSDB; AA018679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.2%; Score 566.4; DB 15; Length 3461; 93.5%; Pred. No. 1.4e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA coding a Non-A, non-B hepatitis virus antigen - useful for detecting HCV within serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus #4 and #6 genes were isolated (AAQ64068-69) Both genes contain the core, ENV, NS1, NS2 and NS3 regions. A core region fragment is given in AAQ64067.
                                                                                                                                                     non-B hepatitis virus; NANBHV; hepatitis C virus; HCV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3461 BP; 638 A; 1046 C; 1012 G; 765 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                       core; ENV; NS1; NS2; NS3; antigen; detection; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TONEN CORP. ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "NS3 N-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1-5; Page 11-15; 22pp; Japanese.
                                                                                                              Non-A, non-B hepatitis virus gene #4.
                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SANW ) SANWA KAGAKU KENKYUSHO CO.
BP.
AAQ64068 standard; cDNA; 3461
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/label= NS2-3
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/label= core
880..1455
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/label= ENV
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Matches 591; Conserv
                                                                                                                                                                                                             Hepatitis C virus.
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ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAAGTGGTCGCCTA
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                                                                                                                                                                                                                                                                                                   242 GGAACGCCAGCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGG
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                                                                                                                                                                                                                                       TGCCCGGTTGCTCTTCTTCCTTCTTGGCTTTACTGTCTGACCATTCCAG
                                                                                        The sequences given in AAT30386-87 encode the 5'UTR/CORE/ENV/NS1/NS2/NS3 protein region derived from hepatitis C virus (HCV) isolates #4 and #6 respectively. The proteins encoded by these sequences particencode amino acids 384-495 of the HCV NS1 antigen. These protein fragments may be used in the detection of antibodies against HCV.
                                        Recombinant polypeptide comprising partial NS1 region of hepatitis non-A non-B viral antigen - used in a method for detecting antibodies against hepatitis non-A non-B virus.
                                                                                                                                                            Length 3461;
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                                                                             Disclosure; Page 10-12; 15pp; Japanese
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                     WPI; 1995-220780/29.
P-PSDB; AAR98361.
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GCGTTCGGGAGAACAACTCTTCCCGGTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTA
                                                          GGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGCGG
                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus; HCV; antigen; detection; antibody; ds.
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/product= Core peptid
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/product= NS1/ENV2
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/product= ENV1
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/product= NS2
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                                 1147 CTGCTTTCTGCTCCGCTATGTACGTGGGGGATCTCTGCGGGATCTGTTTCCTCGTCTCCC
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                                                                                                                                 ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cuticle protein 1 and 2 secreting hepatitis C virus related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19; Length 2187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cuticle protein 1 and 2 secreting hepatitis C virus (Japanese)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to cuticle protein 1 and 2 secondepatitis C virus. The present sequence is a coding sequence provided in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cuticle protein 1; cuticle protein 2; hepatitis C virus; ds
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/product= "AAM47264"
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P-PSDB; AAM47264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the genome of the non-A, non-B hepatitis virus (NANBHV) strain HC-J4. This sequence was derived by amplification by polymerase chain reaction. The nucleotide sequences derived from this amplification can be used to detect NANBHV infection which could not be detected by conventional methods. The detection which could highly specific and sensitive detection at an early phase of infection. The polypeptide product of this coding sequence can be use for the manufacture of vaccines and immunological pharmaceuticals and also to produce antibodies specific to NANBHV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCCCGGTTGCTCTTTCTCTTTCTTTGGCTTTACTGTCCTGTCTGACCATTCCAG
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                                                                                              amplification
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                                                                                           non-B hepatitis virus; NANBHV; PCR; ampill
rase chain reaction; vaccine; antibody; ss.
                                                             NANB hepatitis virus strain HC-J4 genome
                                                                                                                                                                             Location/Qualifiers
342..1880
/*tag= a
/label= HC-J4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 11; 42pp; English.
                                                                                                                                             Non-A, non-B hepatitis virus
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                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      (IMMO ) IMMUNO JAPAN INC
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P-PSDB; AAR24087.
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Best Local Similarity
Matches 590; Conserv
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Best Local Matches 59

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                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of NANB hepatitis virus polynucleotide N-2540-2 which codes for a non-A, non-B (NANB) hepatitis virus gene HC-OM. The polypeptide it encodes may be used in a system for detecting NANB hepatitis. This method is highly specific and sensitive, and can detect NANB hepatitis virus which could not be detected by conventional methods.
                                                                                                        Antigen related to non-A and non-B hepatitis virus - comprises non-translation region comprising 340 - 341 mols. of nucleotides, non-translation region comprising 1885 - 2551 mols. of nucleotides including region 1,149 and, etc.
                                                                                                                                                                                                                                                                                 DB 14; Length 2540;
                                                                                                                                                                                                                                                                               Query Match

88.1%; Score 565.4; DB 14; Length
Best Local Similarity 93.5%; Pred. No. 2.4e-152;
Matches 590; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                            Sequence 2540 BP; 471 A; 775 C; 741 G; 553 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTAAGGTTTTGATTGTGATGCTACTCTTTGC 632
                                                                                                                                                                 Claim 3; Page 19-20; 73pp; Japanese
       91JP-0196175
                          90JP-0153401
90JP-0304405
                                                                                1993-199637/25
                                                          (NAKA/) NAKAMURA T.
                                                                                 WPI; 1993-199637/;
P-PSDB; AAR38279.
         10-APR-1991;
                             12-JUN-1990;
08-NOV-1990;
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342..2540
/*tag= a
1..341
/*tag= b
/*tag= b
/note= "from 5' terminal of NANBH virus RNA"
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             Indels
    Pred. No. 2.2e-152;
0; Mismatches 41;
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      93.5%;
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      al Similarity 93.5
590; Conservative
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1387 CGGGGCCCACTGGGGAGTCCTGGCGGCCTTGCCTACTATTCCATGGTAGGAACTGGG 1446
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                                              .207 AGCTGTTCACCTTCTCGCCTCGCCGCATGAGACAGTGCAGGACTGCACTGCTCAATCT
                                                                                                                                                        1267 Arccceccarriarcaccrcaccardecrressararcarcardateraccaecra
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     362 AGCIGITCACCAICICGCCTCGCCGGCAIGAGACGGIGCAGGACIGCAAIIGCICAAICI
                                                                                                         422 ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA
                                                                                                                                                                                                              482 CAACGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG
                                                                                                                                                                                                                                                                                                                  542 CGGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCV; ds; Con 1; adaptive mutation; liver failure; cirrhosis;
hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
internal ribosome entry site; IRES; NS5A; HCV replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "HCV polyprotein"
/note= "The polyprotein consists of the Core, E1,
E2, P7, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins"
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342..9374
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                                                                                                                                                                                                                                                                                                                                        Polymerase chain reaction; PCR; primer; amplify; detection; NANBHV; non-A, non-B hepatitis virus; 5'-terminal region; core protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer pairs specific for non-A, non-B hepatitis virus - used for high sensitivity detection of non-A non-B (NANB) hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 565.4; DB 15; Length 2540;
Pred. No. 2.4e-152;
0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2540 BP; 470 A; 775 C; 742 G; 553 T; 0 other;
1447 CTAAGGTCCTGATTGTGGCGCTACTCTTCGC 1477
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                                                                                                                               AAQ63753 standard; cDNA to mRNA; 2540
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il Similarity 93.5%;
590; Conservative
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                                                                                                                                                                                                                                                                                     genomic fragment #2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NAKA/) NAKAMURA T.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                            RESULT 1. AAQ63753 AAQ6375 AAQ
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exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing control and the human hepatoma cell the altered nucleic acids; (4) producing an eff of the human hepatioma cell the altered nucleic acids; (4) producing an eff of the human hepations and the end of the containing a control of the control of the containing and the control of the containing and the control of the containing and control of the control of the control of activity. The HCV replicons and HCV replicon enhanced cells made in the control of the co
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 88.1%; Score 565.4; DB 24; Length 9605; Best Local Similarity 93.5%; Pred. No. 3.9e-152; Matches 590; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                           Sequence 9605 BP; 1910 A; 2883 C; 2733 G; 2079 T; 0 other;
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Search completed: December 19, 2003, 18:51:00 Job time : 182.486 secs

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| 40.4 6.3 590 40.4 6.3 645 40 6.2 525 40 6.2 671 | 12 BJ536071 13 BX35664 9 AA459034 14 CAB16001 | 39 6.1 624 12 BI723734 38.6 6.0 399 9 AV638521 38.6 6.0 434 9 AV637507 | 38.6 6.0 451 9 AV63/383 38.6 6.0 451 9 AV63/328 | 38.6 6.0 453 9 AV634724 38.6 6.0 454 9 AV637050 | 38.6 6.0 473 9 AV635382 | 38.6 6.0 481 9 AV6325U3 38.6 6.0 485 9 AV6328II | 38.6 6.0 508 9 AV634243 38.6 6.0 508 9 AV634095 38.6 6.0 526 9 AV641895 | 38.6 6.0 533 9 AV638125 38.6 6.0 537 9 AV632335 38.6 6.0 588 9 AV387329 38.2 6.0 431 9 AV639153 | 38.2 6.0 501 9 AV638474 38 5.9 742 13 BQ752673 | 35 37.8 5.9 1195 28 B10902 36 37.8 5.9 435 14 C72860 37 37 8 5.9 634 10 BETAGEGI | 3/ 3/,8 5.9 634 IO BE/395591 38 37.4 5.8 497 9 AV633658 39 37.4 5.8 856 29 BZS78381 | 37.4 5.8 872 29 BZ555011 37.2 5.8 888 10 BG355821 37.2 5.8 1901 13 BY350106 | 37 5.8 610 14 CB657655 37 5.8 945 29 CNS057WQ | 35.8 5.7 43.1 9 AV636681 | | AV755731 488 bp mRNA linear | 4 Homo sapiens cDNA clone BMFAKB(| AV/52 S EST. | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; But Mammalla; Butheria; Primates; Catarrhini; Hominidae; H 1 (hanga 1 to 400) | Y., Peng, Y., Song, F. | Jarry, Xu.S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,W. Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and C. Homo appiens cDNA BM clones | | 351 Guo Shoujing Road Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. P. | Tel: 86-21-50801921(ex.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai. FEATURES Location/Qualifiers |
|--|--|--|--|--|---|---|---|--|---|--|---|---|--|---|-------------|--|-----------------------------------|-----------------|---|------------------------|--|-----------|--|---|
| GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. | OM nucleic - nucleic search, using sw model Run on: December 19, 2003, 18:03:34 ; Search time 1651.58 Seconds | | ct score: nce: | Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 | Searched: 22781392 segs, 12152238056 residues | Total number of hits satisfying chosen parameters: 45562784 | Minimum DB seq length: 0 Maximum DB seq length: 200000000 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries |) *:H | 1: em_estba:* 2: em_esthum:* 3: em_estin:* | | 6: em_estpl:* 7: em_estro:* 8: em_htc:* | 9: gb_est1:* 10: gb_est2:* 11: gh_hr:* | 12: gb_ect3:* 13: gb_ect3:* 14: gb_ect4:* | em_estfun:* | 17: em_gss_hum:* 18: em_gss_inv:* 19: em_gss_pln:* | | | | gb_gss2 | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | SUMMARIES | Result Query No. Score Match Length DB ID Description | C 1 117.2 18.3 488 9 AV755731 C 2 92.6 14.4 492 9 AV758366 AV758366 AV758366 AV758366 AV758366 AV758368 AV7583013 Drosophil |

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307 CICTGIICCGCIAIGIACGIGGGGGAICICIGCGGAICTGICTICCICGICICCCAGCIG
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psHB036xB09f_300663 psHB: Infected hypocotyl soybean host. 48 hpost infection Phytophthora sojae CDNA clone sHB036B09 5, mRNA
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Phytophthora.
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Tel: 540-231-7318
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/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="sHB036B09"
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Plate: 036 row: B column: 09
Seq primer: BK reverse
High quality sequence stop: 534.
Location/Qualifiers
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CD040840.1 GI:30502701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 534)
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Tyler lab
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1 (bases 1 to 492)

2 (Gu,J., Zhao,M., Huang, Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,J., Xu,S., Gu,M., Tu,Y., Jia,J., Fu,G., Fen,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z. Unpublished
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AV758366 AV Homo sapiens cDNA clone BMFAKA03 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Zeguang Han
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="BMFMR03"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BMZ5.8"
/clone_lb="BM"5.8"
/note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
134 c 137 g 97 t 4 others
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/db_xref="taxon:9606"
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∕organism="Homo sapiens"
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905 KSSSSGSVSSGSGSGS 920
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Submitted (12-JUN-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr. - Web: www.genoscope.cns.fr.)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Direction of the Broger of Cancer Genetics at the Roswell Park Cancer Institute in Briffalo, NY. The library is named RPCI-98 and was constructed by partial Ecord disestion of Erosophila DNA provided by the Broge from the isogenic strain v2: cn bw sp, the same strain used for the Broger of the Broger of the Broger and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR1916 of RPCI-98 library from Drosophila melanogaster (fruit AL053013)
/tissue_type="infected host tissue"
/cell_line="P6497"
/dev_sage="48 hour post infection"
/clone_lib="psHB: Infected hypocotyl soybean host. 48 hrs
post infection"
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                                                                                                               /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; USDA-IFAFS:Expression of Phytophthora sojae genes during infection and propagation." 187 c 159 g 87 t
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 2.5;
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590 bp mRNA linear EST 24-NOV-2002 wlm.pk0005.c9 wlml Triticum aestivum cDNA clone wlml.pk0005.c9 5' CA659369
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Triticum aestivum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae, Pooldeae
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1 (bases 1 to 590)

1 (pagey, S.V., Powall, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.

DuPont Wheat cDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     665 SSSSYTTSKSTSASGSGSWSAGGGSGSTGSTSSSSSSSSTSTSSSSVSSGSKSSTBSSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 AGCTGTTCACCATCTCGCCTCGCCGCATGAGACGGTGCAGGACTGCAATTGCTCAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482 CAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG
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                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                           Length 925;
                                                                                                                                                                 511 others
                                                                                                                                                                                                                                                                                                Indels
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                         ch 6.3%; Score 40.6; DB 29;
1 Similarity 15.8%; Pred. No. 5.5;
69; Conservative 165; Mismatches 198;
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                                                                             /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
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Green to 525)
S Grossman, A. Davies, J., Federspiel, N., Harris, E., Lefebvre, P., S Grossman, A. Davies, J., Federspiel, N., Harris, E., Lefebvre, P., Silflow, C., Stern, D. and Surzycki, R. MoDermott, J. P., Silflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vaccular Plants; project phase 2
Unpublished
Contact: Elizabeth H. Harris
DCMB Box 91000
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8164
Fax: 919 613 817
Email: chlamy@duke.edu.
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Chlamydomonas reinhardtii
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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                                                                                                                                                                                                                                                                                                                               411 TTGCTCAATCTATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAA
                                                                                                                                                                                                                                                                                                                                                                            191 SCCCSNCTNCNNNNTNTTNSSSSSSNSNNNTNNNNNSNNSNNSNNNNSSSGSSSNNNNS
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/strain="CC-1690 wild type mt+ 21gr"
                                                                                                                                                                      10.9%; Pred. No. 5.5; ive 85; Mismatches 144;
                                                                                                                                               DB 29;
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                                                                          92
                                                                                                                                               6.3%; Score 40.4;
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
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28; Conservative
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Submission
Submission
Submission
BP 191 91006 EVRY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre of Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genome survey sequence T7 end of BAC BACN08607 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                     /db_xref="taxon:4565"
/clone="wlml.pk0005.cg"
/tissue_lype="leaf"
/clone=lib=wlml"
/note="Vector: pBluescript SK+; Site_l: EcoRI; Site_2:
XhoI; Wheat (Triticum aestivum L.) seedlings 1 hr after
inoculation with Erysiphe graminis f. sp tritici"
a 218 c 159 g 88 t 19 others
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol type="genomic DNA"
/db xref="taxon:7227"
/clone="BACN08C07"
                                                                                                                                                                                                                                                                                                                                            Score 40.4; DB 14;
Pred. No. 5.3;
0; Mismatches 136;
                                          organism="Triticum aestivum"
                                                           /mol_type="mRNA"
/cultivar="Stephens"
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Best Local Similarity 47.3%;
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ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebv, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
                                                                                                                                                                                                                              GCACCGCTTCAACAACCCCACCGTGAATTCGCCCGCCTACAAGTACCTGCTGTCCAT
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1031067F08.yl C. reinhardtii CC-1690, Stress II (normalized)
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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                                                                                                                              Score 40; DB 10; Length 525;
Pred. No. 6.5;
0; Mismatches 140; Indel8
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/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
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Location/Qualifiers
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DCMB Box 91000
Duke University
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                                                                                                                                                                Matches 124; Conservative
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Fax: 919 613 8177
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Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Gd (1, 2, 6, 24 hr).

PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The CDNA was directionally cloned into lambda and II of Caratagene) in the EcoRI (5,) and KhORI (3,) sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Tal: Nishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Coone="MyrolSSB002D03"
/sex="mixture of female and male"
/tissue_type="whole embryo"
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Pred. No. 7.1;
0; Mismatches 140;
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/mol_type="mRNA"
/strain="Hd-rR"
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Kohara,Y., Shin-i,T., Kimura,T., Ne
Medaka EST Project in Takeda's lab
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BJ536071.1 GI:22194883
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ilarity 47.0%;
Conservative (
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/mol type="mRNA"
/db_xref="taxon:9606"
/dlone="CSODIOIDYB03"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCWNSPORT 6 vector. Library was normalized."
6 a 88 c 53 g 39 88 t 506 others
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BX356664 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CS0DI015YB03 3-PRIME, mRNA sequence.
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1 (bases 1 to 1201)
1 id. W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished
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Library was constructed by Life Technologies, a division of
Invircopen. Contact: Feng Liang Email: filangedlifetech.com URL
http://fulllength.invircopen.com/ InVircoGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO15CAO2NP1.
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llarity 13.6%; Pred. No. 8.6;
Conservative 223; Mismatches 264; Indels '
                                                                                                                                      Length 740;
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                         Score 40; DB 12;
Pred. No. 7.3;
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                                /clone_lib="MF01SSB cDNA"
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AAA59034 1.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814365 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 382.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                        CAGCGICCCCACCACGACAATACGACGCCACGICGAITIGCICGTIGGGGGGGGCGCTGCT
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                            STISTISBSSSITITITSBISSSISBSBIISCTITIKSBSSSTBSTBSTISTBS
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/db_xref="GDB:603252"
/db_xref="taxon:9606"
/clonne="InAGE:814365"
/lisue_type="germinal center B cell"
/lab_hogt="DH10B"
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/organism="Homo sapiens"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Vitaceae; Vitis.
Vitaceae; Vitis.
Goses 1 to 621)
Goes da Silva,F., Lim,H., Iandolino,A., Baek,J., Jones,K., Walker,M.A. and Cook,D.R.
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]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
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/note="Organ: Leaf; Vector: pDNR; Site_1: Sfi1; Site_2:
Sfi1; CAl2EI is a cDNA library of Cabernet Sauvignon—
leaves. The leaves were collected on July 25, 2001, in
Napa Valley, California, and represent leaves in
mid-season development. These leaves were verified to be
infected with the bacterial pathogen, Xylella fastidiosa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCAC 432
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                                                                                                                                                                                                                                                                                                Length 423;
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/lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                Score 39.6; DB 9;
Pred. No. 7.8;
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/cultivar="Cabernet Sauvignon"
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Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seg primer: GTTATCAGTCGACGGTACC.
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/clone="CA12E13011VF_E04"
/8ex="hermaphrodite"
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Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J. P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031
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/note="Vector: PBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines CDNAs from CC-1690 ealls grown to mid-log phase in TAP (NH+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
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1031067F08.y2 C. reinhardtii CC-1690, Stress II (normalized)
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/strain="CC-1690 wild type mt+ 21gr"
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Location/Qualifiers
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Contact: Charles Hauser
DCMB Box 91000
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).

Polya mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the BCORI (5') and XhORI (3') sites, pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
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/organism="Chlamydomonas reinhardtii"
/mol__type="mmNA"
/strain="C9"
/db_xref="taxon:3055"
/db_xref="taxon:3055"
/clone="thr087407_rein"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: PBluescriptII SK-; Site_2: PBluescriptII SK-; Site_2: PBluescriptII SK-; Site_3: PBl
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AV638521 GI:10781841
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Chiamydomonas reinhardtii
Chiamydomonas reinhardtii
Eukaryota; Viridiplantae: Chlorophyta; Chlorophyceae; Volvocales;
Chiamydomonadaceae; Chlamydomonas.

(hases 1 to 399)
Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.

Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNR Res. 7 (5), 305-307 (2000)
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| Organism="Chlamydomonas reinhardtii"
| forganism="Chlamydomonas reinhardtii"
| mol type="mRNA"
| forzain="C9"
| db xref="teaxon:3055"
| clone="HC074a01 r"
| clone lib="Chlamydomonas reinhardtii 5% CO2"
| clone lib="Chlamydomonas reinhardtii 5% CO2"
| clone lib="Coxtox: pBluescriptII 5K'; Site_1: EcoRI; Site_2: | note="Vector: pBluescriptII 5K'; Site_1: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV637507 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii cDNA clone HC074a01_r 5', mRNA sequence.
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Tontact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarzau, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Sasmizu, E., Mura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Obyama, K., Nakamizu, E., Mura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Obyama, K., Nakamura, Y. and Tabata, S. Generation of expressed sequence tags from low-CO2 and high-CO2 Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii DNA Res. 7 (5), 305-307 (2000)
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(c) 1993 - 2003 Compugen Ltd.
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Sequence 21, 1
Sequence 21, 1
Sequence 21, 1
Sequence 17, 1
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APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARRYNOFF, GU
APPLICANT: BUYSE, MARRIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TOWNER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1
Sequence 2
Sequence 2
Sequence 2
Sequence
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Sequence
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PLING DATE: 11-MAR-1996
CLASSIFICATION (435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32.205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CIRRACTERISTICS:
SEQUENCE CIRRACTERISTICS:
SEQUENCE CIRRACTERISTICS:
                                                                                                                           US-08-324-977-13
US-08-384-616-13
US-08-904-686A-13
US-09-315-850-13
US-08-324-977-1
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US-08-904-686A-1
US-09-315-856-1
US-08-82-895A-27
US-08-066-4288-21
US-08-666-570-21
US-08-290-665A-21
US-08-466-601A-21
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                                                                                           JS-09-315-850-11
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COUNTRY: U.S.A.
ZIP. 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
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ACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCAAGCTGTGTGGACATGGTG 540
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                                                                                                                                                                                LENGTH: 642 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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1..636
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HYPOTHETICAL: NO
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FEATURE:
NAME/KEY: CDS
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US-08-927-597-3
Sequence 3, Application US/08927597
Sequence 3, Application US/08927597
Sequence 3, Application US/08927597
Setent No. 6245503
GENERAL INFORMATION:
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-BANGE
APPLICANGE
APPLICANTES: 111
CORRESPONDENCE ADDRESS: 111
CORRESPONDENCE ADDRESS: 1100 NORTH GLEBE ROAD
STREET: 11100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
STATE: VIRGINIA
STATE: VIRGINIA
                                                                      TGCGTTCGGGAGAACAACTCTTCCCGCTGCGTAGCGCTCACCCCCCACGCTCGCAGCT
                                                                                                                                                                                                     Gaps
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0
                  Length 642;
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                                       Indels
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100.0%; Pred. No. 2.2e-159;
                                       0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
                     Query Match
Best Local Similarity 100.
Matches 642; Conservative
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US-08-612-973-3
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT PAPPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION NUMBER: US 08/612,973
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYREE, THOMAS E.
REGISTRATION NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
TELECOMMUNICATION 1000
TELECOMMUNICATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
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241

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335 GCGTTCGGGAGAAACACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTA 394
                                                                                                                                                                                                                                                                                                                                                                                             515 AGCTGTTCACCATCTCGCCTCGCCGCATGAGACGGTGCAGGACTGCAATTGCTCAAATCT 574
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                                  GGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGG 301
                                                                                                                                                                                                                                                                                            395 GGAACGCCAGCGTCCCCACCACGACAATACGACGCCCACGTCGATTTGCTCGTTGGGGGGG 454
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362 AGCTGTTCACCATCTCGCCTCGCCGGCATGAGGCGTGCAGGACTGCAATTGCTCAATCT 421
                                                                                                                182 GCGTTCGGGAGAACACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTA
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Sequence 5, Application US/08927597

Sequence 5, Application US/08927597

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: MARRIE-ANGE

APPLICANT: BUSBAN, FONS

ITTLE OF INVENTION: PROTFIED HEPATITIS C VIRUS ENVELOPE

ITTLE OF INVENTION: PROTFIED HEP
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602 CTAAGGTTTTGATTGTGATGCTACTCTTTGCTCTCTAATAG 642
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PRIOR APPLICATION DATA:
APPLICATION UNDERS: US 08/612,973
APPLICATION UNDERS: US 08/612,973
FILING DATE: 11-WAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARTYNOFF, GUY
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: ALLANDERS

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSITCATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
RETERENCE/DOCKET NUMBER: 1487-10
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TENTORY: 795 base pairs
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                                                                                                             GCTAAGGTTTTGATTGTGATGCTACTCTTTGCTCTCTAATAG 642
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Pred. No. 9.7e-156;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                       RESULT 3
US-08-612-973-5
; Sequence 5, Application US/08612973
; Patent No. 6150134
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Best Local Similarity 98.8%;
Matches 633; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
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CORRESPONDENCE ADDRESS;
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FEATURE:
NAME/KEY: CDS
LOCATION: 1..7
FEATURE:
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MOLECULE TYPE:
HYPOTHETICAL: N
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; LOCATION:
US-08-612-973-5
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APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOF, GUY
APPLICANT: DE MARTYNOF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF LIVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE D
STREET: 1100 NOP""
                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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FEATURE:
NAME/KEY: CDS
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LOCATION:
US-08-612-973-47
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FEATURE:
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                                                                                                                                                                                                                                            Score 628.2; DB 3;
Pred. No. 9.7e-156;
0; Mismatches 8;
                                           TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEBTURE:
FARTURE:
                                                                                                                                                                                                                                                Query Match 97.9%;
Best Local Similarity 98.8%;
Matches 633; Conservative
                                                                                                                                                                                                        mat_peptide
1..789
                                                                                                                                                                                    1..792
                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                    LOCATION:
US-08-927-597-5
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CTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTTCCC 361 ö GGAACGCCAGCGTCCCCACCACCACACACGCCCACGTCGATTTGCTTCGTTGGGCCGG 301 334 241 121 274 182 GCGTTCGGGAGAACAACTCTTCCCGCTGGGTAGCGCTCACCCCCACCCTCGCAGCTA Gaps .. 0 Length 2082; STREET: ALLUCATORION
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
ZIP: 22201-4714
ZIP: 22201-4714
ZOMPUTER READABLE FORM:
MEDIUM TYED: FIDPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
TILING DATE: 11-MAR-1996
TLASSIPICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
TLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOWARS E: 1487-10
TELEFRAK: (703) 816-4100
TELEFRAK: (703) 816-4100
TELEFRAK: (703) 816-4100
TELEFRAK: (703) 816-4100
TELEFRAK: USOR ED DASE PATE
SEQUENCE CHARACTERISTICS:
LENGTH: 2082 base Paire Indels DB 3; Query Match
Best Local Similarity 98.9%; Pred. No. 1.9e-153; Matches 624; Conservative 0; Mismatches 7; 302 d ò

RESULT 5
US-08-612-973-47
; Sequence 47, Application US/08612973
; Patent No. 6150134
; GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                            2 IGCCCGGTTGCTCTTTCTCTTTCTTTCTTTGGCTTTACTGTCCTGTCTGACCATTCCAG
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APPLICANT: MARRIENS, GEERT
APPLICANT: BORNAN, FONS
APPLICANT: BUSSE, MARITORF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PORTFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FON DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                               .
                                                                                                                                                             Length 2082;
                                                                                                                                                                                                                               Indels
                                                                                                                                                          96.5%; Score 619.8; DB 3;
98.9%; Pred. No. 1.9e-153;
iive 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 CTAAGGTTTTGATTGTGATGCTACTCTTTGC 632
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                                                                                                                                                                                         Best Local Similarity 98.9
Matches 624; Conservative
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                           ; NAME/KEY:
; LOCATION:
US-08-927-597-47
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455 CTGCTTTCTGTTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCC 514
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                                                                                                   515 AGCTGTTCACCATCTCGCCTCGCCGCATGAGACGGTGCAGGACTGCAGATTGCTCAATCT
                                                                                                                                                                                         422 ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA
                                                                                                                                                                                                                                                                                                                                                                                         635 CAACGGCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG
                                                                                                                                                                                                                                                                                                                           CAACGCCCTGGTGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARTYNOFF, GUY
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/927,597
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CLLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 47, Application US/08927597
Patent No. 6245503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..2079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
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NAME/KEY:
LOCATION:
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US-08-927-597-47
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CGGGGGCCCAITGGGGAGTCCTGGCGGCCTCGCCTACTATTCCATGGTGGGAACTGGG 601
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HERATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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Pred. No. 2e-153;
0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                            1106 CTAAGGTTTTGGTTGTGATGCTACTCTTTGC 1136
                                                                                                                               632
                                                                                                                               CTAAGGITTTGATTGTGATGCTACTCTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEFAN: (703) 816-4100
TELEFAN: (703) 816-4100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2433 base pairs
TYPE: NUCleic acid
TYPE: NUCleic acid
TYPE: NUCleic acid
                                                                                                                                                                                                                                                                                                           US-08-927-597-49; Sequence 49, Application US/08927597; Patent No. 6245503; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.9%;
Matches 624; Conservative C
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NAME/KEY:
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LOCATION:
US-08-927-597-49
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                                                                                                                                  OPERATIG SYSTEM: PC-DOS/MS-UUS
SOFTWARE: PATENTIN RELEAGE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 1.-MR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THORMATION:
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION S16-4100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2433 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ANTICENSE: CDNA
ANTICENSE: AND
                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches 624; Conservative
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                                      COMPUTER READABLE FORM:
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LOCATION:
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Sequence 14, Application US/08470426B
Patent No. 5885458
GENERAL INFORMATION:
APPLICANT: Okamoto, Hiroaki
APPLICANT: Nakamura, Tetsuo
ITILE OF INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR
ITILE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-B
ITILE OF INVENTION: HEPATITIS VIRUS
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                                                                                                                                                                                                                                                                                               Length 1539;
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                                                                                                                                                                                                                                                                                           Query Match 87.8%; Score 563.8; DB 2; Best Local Similarity 93.3%; Pred. No. 8.7e-139; Matches 589; Conservative 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTAAGGTCCTGATTGTGGCGCTACTCTTCGC 1136
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                            06/59-47083.1
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                   REFERENCE DOCKET NUMBER: 06/5;
FELECOMMUNICATION INFORMATION:
FELEPHONE: (202) 659-2811
FELEPHONE: (202) 659-281
FELEPHONE: (202) 659-1462;
FINFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1539 base pairs
FYPE: nucleic acid
STRANDEDNESS: single
FYPE: nucleic acid
TYPE: nucleic acid
FYPE: nucleic acid
FYPE: nucleic acid
STRANDEDNESS: single
FYPE: DAA (Genomic)
US-08-470-4268-17
        20,531
                                                                                                                                                                                                                                                                                                                                                                               2 TGCCCGGTTGCTCTT1
        REGISTRATION NUMBER:
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US-08-470-426B-14
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Patent No. 5856458
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Okamoto, Hiroaki
APPLICANT: Nakamura, Tetsuo
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR
TITLE OF INVENTION: HEPATITIS VIRUS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               986 CAACGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG 1045
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                                                                   GCGTTCGGGAGAACACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTA
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                                                                                          626 ACTCAAGCATTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCCGGGTGCTGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CITY: Washington
STATE: DC
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-153402
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Weilacher, Robert G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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Sequence 18, Application US/08081072

Sequence 18, Application US/08081072

Patent No. 5641654

GENERAL INFORMATION:
APPLICANT: No. 5641654cru MAKI, Kenjiro YAMAGUCHI, Ayumi, APPLICANT: TOYOSHIMA, and Michinori KOHARA

TITLE OF INVENTION: NON-A NON-B HEPATITIS.SPECIFIC

TITLE OF INVENTION: ANTIGEN AND ITS USE IN HEPATITIS

TITLE OF INVENTION: DIAGNOSIS

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 130 Water Street
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Pred. No. 1.3e-137;
0; Mismatches 45; Indels
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ZIP: 02109-4280
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk,3.50inch,1.4Mb storage
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Macintosh Classic
SOFTWARE: Microsoft Word Version 4.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081.072
FILING DATE: June 22, 1993
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: acid
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Local Similarity 92.9%;
nes 586; Conservative
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COUNTRY: USA
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Pred. No. 9.1e-139;
0; Wismatches 42; Indels 0:
                                                                     ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young, ADDRESSEE: L.L.P. STREET: 1850 M Street, N.W., Suite 800 CITY: Waghington
                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Flopped disk

MEDIUM TYPE: Flopped disk

COMPUTER: IBM PC compatible

COMPUTER: ISON 1995

FILING DATE: 06-40N-1995

FILING DATE: 12-40N-1990

ATTONEY/AGENT INPORMATION:

ANNER: ACCOUNTER: DP 2-153402

FILING DATE: 12-40N-1990

ATTONEY/AGENT INPORMATION:
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Best Local Similarity 93.3%;
Matches 589; Conservative (
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STRANDEDNESS: single
                             NUMBER OF SEQUENCES: 3.
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                                                                                94 TGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCCTGTTTGACCATCCCAG 153
                                                                                                                                                                                                                                          154 crrccccrrarcancerececancerarccescararaccarereaceaceaceacrecie 213
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Betent No. 5641654

GENERAL INFORMATION:
APPLICANT: No. 5641654 and Michinori KOHARA
TITLE OF INVENTION: NON-A NON-B HEPATITIS-SPECIFIC
TITLE OF INVENTION: ANTIGEN AND ITS USE IN HEPATITIS
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk,3.50inch,1.4Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh Classic
SOFTWARE: Microsoft Word Version 4.0A
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APPLICATION NUMBER: US/08/081,072
FILING DATE: June 22, 1993
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 Water Street
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Patent No. 5662906
GENERAL INFORMATION:
APPLICANT: No. 5662906oru MAKI, Kenjiro YAMAGUCHI, Ayumi
APPLICANT: TOYOSHIMA, and Michinori KOHARA
TITLE OF INVENTION: ANTIGEN AND ITS USE IN HEPATITIS
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Dike, Bronstein, Roberts & Cushman, LLP
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STREET: 130 Water Street
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COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTEEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,093A
FILING DATE: May 24, 1995
CLASSIFICATION: 424
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APPLICATION DATA:
APPLICATION NUMBER: 08/081,072
FILING DATE: June 22, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/726,141
FILING DATE: July 8, 1991
CLASSIFICATION: 424
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 92.5
Matches 586; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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MOLECULE TYPE:
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                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFFWARE: FastERO Version 1.5
SOFFWARE: FastERO Version 1.5
SOFFWARE: FastERO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,093A
FILING DATE: MAY 24, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/081,072
FILING DATE: June 22, 1993
CLASSIFICATION: 424
PRICA PARTICATION NUMBER: 07/726,141
PRICA PAPLICATION: 424
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 932 base pairs
LENGTH: 932 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLLOGY: linear
MOLECULE TYPE: CDNA to genomic RNA
ZIP: 02109-4200
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local &
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. 5662906cru MAKI, Kenjiro YAMAGUCHI, Ayumi
APPLICANT: No. 5662906cru MAKI, Kenjiro YAMAGUCHI,
TITLE OF INVENTION: NON-A NON-B HEPATITIS-SPECIFIC
TITLE OF INVENTION: ANTIGEN AND ITS USE IN HEPATITIS
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSED: Dike, Bromstein, Roberts & Cushman, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                     Score 559; DB 1; Length 932;
Pred. No. 1.4e-137;
0; Mismatches 45; Indels
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; Sequence 15, Application US/08449093A
; Patent No. 5662906
                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
                                                                                                                                                                                                                                       87.1%;
92.9%;
                           LENGTH: 932 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 92.9
Matches 586; Conservative
      SEQUENCE CHARACTERISTICS:
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STREET: 13(
CITY: Bost
STATE: Mass
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639 541

579 481

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301 459

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Query Match 86.6%; Score 555.8; DB 3; Length 2116; Best Local Similarity 92.6%; Pred. No. 1.2e-136; Matches 584; Conservative 0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy diskette, 5.25 inch, 360 Kb storage
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COCATION: polyprotein
OTHER INFORMATION: viral structural and non-structural
STHER INFORMATION: proteins
US-08-191-160-21
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TYPE: nucleotide with corresponding protein
STRANDEDNESS: single
760 CTAAGGTTTTGATTGTGATGCTACTCTTCGC 790
                                                                                                                                              Sequence 21, Application US/08191160
Patent No. 6210675
GENERAL INFORMATION:
APPLICANT: Highfield, Peter Edmund
APPLICANT: Tedders, Brian Colin
APPLICANT: Tedders, Brian Colin
APPLICANT: Barbara, John Anthony James
TITLE OF INVENTION: Viral Agent
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
                                                                                                                                                                                                                                                                                                                                                                                                          Rothwell, Figg, Ernst & Kurz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION NUMBER:
70/628,516
FILING DATE: 17 DEC 1990
APPLICATION NUMBER: UK 89 28 562.1
FILING DATE: 18 DEC 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 90 04 414.0
FILING DATE: 27 FEB 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 90 04 814.1
FILING DATE: 07 REB 1990
ATTORNEY/AGENT INFORMATION:
NAME: E. ALTHONY Figg
REGISTRATION NUMBER: 27,195
REGISTRATION NUMBER: 1645-103A
TELECOWMUNICATION INFORMATION:
TELECOWMUNICATION INFORMATION:
TELEPHONE: (202) 833-5740
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: human; serum infectious for IMMEDIATE SOURCE:
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OPERATING SYSTEM: MS-DOS V3.2
SOFTWARE: Wordperfect 5.0 (DOS text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,160
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ORIGINAL SOURCE:
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20006
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.053 AGGACGCCAGCATCCCCACTGCGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCCGG 1112
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                                                    182 GCGTTCGGGAGACAACTCTTCCCGCTGCTAGGGTAGCGCTCACCCCCACGCTCGCAGCTA 241
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813 TACCCGGTTGCTCTTTCTCTTTCCTCTTTGGCTTTTGCTGTCTGTTTGACCATTCCAG 872
                                                                                                                              CTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTTGCGGGATCTGTCTTCCTCGTCTCCCC
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Search completed: December 20, 2003, 07:02:57 Job time : 49.3008 secs

TGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTACTGTCCTGTCTGACCATTCCAG

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December 19, 2003, 16:55:48; Search time 3010.09 Seconds (without alignments) 10804.703 Million cell updates/sec 795 1 AIGTIGGGIAAGGICAICGA.....TACICITIGGICCCTAAIAG 795 5777422 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 2888711 segs, 20454813386 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-09-899-303A-5 GenEmb1:* Title: Perfect score: Sequence: Scoring table:

Searched:

Run on:

em_htgo_mus:* em_htgo_other:* em un: *
em vi: *
em htg hum: *
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em htg other: *
em htg mus: *
em htg pln: * em_htg_mam: * em_htg_vrt: * em_sy: * em_htgo_hum:* em_fun:* em_hum:* em_in:* em_mu:* em_ph:* em_pl:* em_ro:* em_sts:* gb htg: *
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gb ov: *
gb pt: *
gb pr: *
gb re: * em_pat:* em_or:* em om: Database :

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | A48667 Sequence 5 AR157325 Sequence AX45274 Sequence AX48700 Sequence A487795 Sequence AX157796 Sequence AX685048 Sequence AX685048 Sequence AX685048 Sequence AX6850795 Sequence AX6850795 Sequence AX6850795 Sequence AX6850798 Sequence AX4577951 Sequence AX4577951 Sequence | AX685050 Sequence AF207766 Hepatitis AJ000009 Hepatitis AJ12296 Hepatitis AF155056 Hepatitis AF155056 Hepatitis AF165054 Hepatitis AB008441 Hepatitis AB008441 Hepatitis AF165054 Hepatitis AF207761 Hepatitis AF207761 Hepatitis AF207761 Hepatitis | AB008446 Hepatitis AB15051 Hepatitis AB049101 Hepatitis AB049101 Hepatitis AB049091 Hepatitis AX739971 Sequence AX03625 Sequence AX03625 Sequence AX03626 Sequence D0083 Hepatitis D10867 Hepatitis A74813 Hepatitis A74813 Hepatitis A74813 Hepatitis A74813 Hepatitis A74813 Hepatitis | NA linear PAT 07-MAR-1997 Buyse, M. PROTEINS FOR DIAGNOSTIC AND |
|---------------------------|--|--|--|---|
| OB ID | 6 A48667 6 AR157325 6 AX452754 6 AX685006 6 A48709 6 AX157750 6 AX422796 6 AX685048 6 AX685048 6 AX6711 6 AX157798 | 6 AX685050 14 AF207766 14 HCV132996 14 AF165055 14 AF165055 14 HPCK1R2 14 HPCK1R2 14 AB008441 14 AF207761 14 AF207761 | ५५५५५ ५ ५ ५५५५५ | 795 bp D t W09604385. ', De,M.G. and VIRUS ENVELOPE 5 15-FEB-1996; |
| % Query e Match Len | 100.0 79 100.0 100 | 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | 2.2 88.7 3296 6.6 88.5 3296 6.6 88.5 3296 6.6 88.5 9547 6.6 88.5 9605 6.6 88.5 11076 6.6 88.5 11076 6.6 88.5 11076 7.7 10.0 10.0 10.0 10.0 10.0 10.0 10.0 1 | A48667 Sequence 5 from Paten A48667 A48667.1 GI:2302380 unidentified unidentified unidentified unidentified The Base 1 to 795) Maextens, G., Bosman, F PURIFIED HEPATITIS C THERAPEUTIC USE PATENTIS C THERAPEUTIC USE PATENTIS C |
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(Lases 1 to 795)

(Lases 1 to 795)

Maettens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.

Maettens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.

Purified hepatitis C virus envelope proteins for diagnostic therapeutic use

Patent: US 624503-A 5 12-JUN-2001;

Location/Qualifiers
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Other publication CA 2172273 960215
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/procein_id="Cad86520.1"
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/translation="MLGKVIDTLITCGFADLVGYIPLVGAPLGGAARALAHGVRVLEDG
VNYATGAHECGSFSIPELALLSCLITVPASAYEVRNVSGWYHVTNDCSNSIVYEADDM
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Purified Hepatitis C Virus envelope proteins for diagnostic
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/note="unnamed protein
/codon_start=1
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/organism="Hepatitis C
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| mol_type="genomic DNA"
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| OLGSVFLVSQLFTISPRRHETVQDCNCSIYPGHITGHRAMDNAMNNASPTTALVVS
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Maertens, G., Bosman, F., De, M.G. and Buyse, M.
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QLLRIPQAVVDWVAGAHWGALAGLAYSWSWVGNWAKVLVVMLLPAGVDGHTRVSGGAAA
SDTRGLVSLFSPGGAQKIQLVNTGSWHINRTALNCNDSLQTGFFAALFYKHKNSSG
CPBRLASCRSIDKFAQGWGPLTYTEPNSSDQRPYCWHYAPRPCGIVPASQVCGPVYCF
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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VNYATGNLPGCSFSIFLLALLSCLTVPASAYEVRNVSGMYHVTNDCSNSSIVYEAADM
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                                                    ATGATCATGCACCCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGCTGC
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/db_xref="GI:21712482"
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/mol_type="genomic DNA"
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
                                                    CGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG
                                                                                                GACCTCTGCGGGTCTTCCTCGTCTCCCCAGCTGTTCACCATCTCGCCTCGCCCGGCAT
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Purified Hepatitis C Virus envelope proteins for
therapeutic use
Patent: WO 02055548-A 47 18-JUL-2002;
INNOGENETICS N.V. (BB) DNA Score 778.8; DB 6; Pred. No. 1.3e-163; 0; Mismatches 2; 9 Hepatitis C virus Hepatitis C virus Viruses; SSRNA positive-strand viruses, Hepacivirus. DNA virus" 482 2082 bp 1 from Patent WO02055548. 1.2082, vocatifies C vi /organism="Hepatitis C vi /mol_type="genomic DNA" /db xref="taxon:11103" Location/Qualifiers 1. .2076 /product="unnamed" 634 c 600 g 98.0%; nilarity 99.7%; Conservative 0 GI:29371453 LLALPPRAYA" Query Match Best Local Similarity Matches 780; Conserv AX685048 Sequence 47 f AX685048 AX685048.1 C 366 mat_peptide 364 184 184 244 304 304 4 4 64 64 124 124 BASE COUNT ORIGIN source LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL REFERENCE CDS FEATURES X685048 QQ 요 ò ద ò g Š g. ò g ò ò 8

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Pred. No. 1.3e-163;
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Sequence 49 from patent US 6245503.
AR157351
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Local Similarity 99.7%;
Nes 780; Conservative
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MIMTPGCVPCYRENNSSRCWALTIPLLARNASVPTTTIFRHVDLLVGAAAFCSAMY
WGDLCGSVFLVSQLFTISPRHETVQDCNGSIYPGHTTGHRWAMDMMNWSPTTALVV
SQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLVVMLLFAGVDGHTRVSGGGAA
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GCPERLASCRSIDKFAQGWGPLFYTEPNSSDQRPYCWHYAPRPCGIVPASQVCGPVYC
FTPSPVVVGTTDRFGVPTYNWGANDSDVLILNNTRPPRGNWFGCTWMNGTGFTKTCGG
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SRPSWGPTDPRRRSRNLGKVIDTLTCGFADLVGYIPLVGAPLGGAARALAHGVRVLED
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TIFKVRMYVGGVEHRFEAACNWTRGERCDLEDRDRSELSPLLLSTTEWQILPCSFTTL
PALSTGLIHLHQNIVDVQYLYGVGSAVVSLVIKWEYVLLFLLLADARICACLMMMLL
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1 (bases 1. Co. 2433)

Maertens, G., Bosman, F., De, M.G. and Buyse, M. PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND
                                                                                                                                                                                      GACCTCTGCGGGATCTGTCTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGGAT
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'note="unnamed protein product"
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Patent: WO 9604385-A 49 15-FEB-1996;
INNOCENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.
Location/Qualifiers
1. 2433
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Sequence 49 from Patent WO9604385.
A48711
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/db_xref="GI:2302425"
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/ GOOD ECRETE 1
/ GOOD FEATURE 12171248 ##
/ AB XTEF = 10.112140 ##
/ AB XTEF = 10.112140 ##
/ AB XTEF = 10.112170248 ##
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Meertens,G., Bosman,P., de Martynoff,G. and Buyse,M.A.
Recombinant vectors for producing hov envelope proteins
Patent: EP 1211315-A 49 05-UUN-2002;
Innogenetics N.V. (BB)
Location/Qualifiers
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Pred, No. 1.3e-163;
0; Mismatches 2;

    . 2430
/note="unnamed protein product"

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Hepatitis C virus
Viruses; ssRNA positive-strand viruses,
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Sequence 49 from Patent EP1211315.
AX452798 AX452798.1 GI:21712483
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/organism="Hepatitis C vi
/mol_type="genomic DNA"
/db_xref="taxon:11103"

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/product="unnamed"
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
purified hepatitis C virus envelope proteins for diagnostic and
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Hepacivirus.
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                               GACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT
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Patent: WO 02055548-A 49 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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WO02055548.
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                                                                                                                                                                                                                                                                      Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Direct Submission
Direct Submission
Submitted (23-NOV-1999) Second Department of Internal Medicine,
Submitted (23-NOV-1999) Second Department of Internal Medicine,
Tokyo Medical and Dental University, 1-5-45 Yushima Bunkyo-ku,
Tokyo 113-8519, Japan
Tokyo 113-8519, Japan
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                  AF207766 9379 bp RNA lin
Hepatitis C virus strain MD25 complete genome.
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ARDYSKALMRVAABEYVEVTRVGDFHYVTGMTTDNVKCPCQVPAPEFFTEVDGVRLHR
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Direct Submission
Submitted (02-UU-1997) Trowbridge R., Hepatitis Unit, Sir Albert
Sakzewski Virus Research Centre, Royal Children's Hospital, Herston
Road, Brisbane, Queensland Q 4029, AUSTRALIA
Location/Qualifiers
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VRL 15-JAN-1999
                                                                                                                                                                                                                                                                                                                                                           AJ000009.1 GI:2764397
complete genome; core protein; El protein; E2 protein; NS2 protein;
NS3 protein; NS4a protein; NS4b protein; NS5a protein; NS5b
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LQVWIPPLNVRGGRDAIILLTCVVHPELIFDITKLLLAMLGPPMVLQAVITKVPYFVR
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AYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSK
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MRSPVFTDNSSPPAVPETFQVAHLHAPTGSGKSTKVPAAXAAQGYKVLVLNPSVAATL
GFGAYMSKAHGTDPNIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIIICDECHS
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Trowbridge, R. and Gowans, B.J.
Molecular cloning of an Australian isolate of hepatitis C virus
Arch. Virol. 143 (3), 501-511 (1998)
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/note="genomic RNA for polyprotein precursor, complete
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Hepatitis C virus complete genome sequence.
AJ000009
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DHLEFRESVETGLTH DAHFLEGTKÖAGENFPYLTAYOATVCKRAQAPPPSWDGWWKC
LIRLKPTLHCPTPLLYRLGAVONEVULTHPTTKY IMACWSADLEVVTSTWULVGGVLA
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TLTCYLKASAACRAAKLODCIMLVCGDDLVVICESAGTOEDAASLRVFTEAMTRYSAP
PGDPPQPEYDLELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNS
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LHGILSAFSLHSYSPGBINRYASCLRKLGVPPLRVWRHRARSVRAKLILSRGGRAATCGK
YLFNWAVRTKLKLTPIPAASRLDLSGWFVAGYSGGDIYHSLSPARPRWFUMCLLLLSV
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RVGESIYQCCDLAPEARQAIRSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGN
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2 (bases 1 to 9418)
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Submitted (07-MAR-1999) Rispeter K., Universitaetsklinikum Essen,
Submitted (107-MAR-1999) Rispeter K., Universitaetsklinikum Essen,
Institut fuer Virologie, Hufelandstrasse 55, 45122 Essen, GERMANY
Location/Qualifiers
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/organism="Hepatitis C virus"
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GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC 303
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             TGGGTAGCGCTCACCCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACAATA
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/isolate="HCV-AD78"
/db_xref="taxon:11103"
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TTGGCTTTGCTGTCTGTCTGACCGTTCCGCTTTCGCTTATGAAGTGCGCAACGTGTCC 243
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Copyright (c) 1993 - 2003 Compugen Ltd.
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| \$ 2 3 | HCV; E1; serotype | ш. | 6 | | de b | ond | phide bond cleavage; phase hybridisation | envelope protein; assay; genotype; | ; vaccine; human; antigen; sera; |
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| SO | Hepatitis | itis C | virus | us. | | | | | |
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Purifying recombinant hepatitis C virus (HCV) El and El envelope

Maertens G;

De Martynoff G,

WPI; 1996-129401/13

Bosman F,

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                                                                 AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1 and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins on then be isolated using a method of the The recombinant proteins and then be isolated using a method of the carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used to vaccinating humans against HCV, for in vitro detection of HCV for vaccinating humans against HCV, for in vitro detecting one or antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated contour second phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and conformation method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and are more reactive with human sera than those isolated by known
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proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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100.0%; Score 795; DB 17; Length 795;
Best Local Similarity 100.0%; Pred. No. 3.6e-204;
Matches 795; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                Sequence 795 BP; 130 A; 240 C; 231 G; 194 T; 0 other;
                                                       Claim 23; Fig 21; 146pp;
                                                                                                                                                                                                                                                                                   techniques.
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                                                                                    CTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus clone HCCI10A El protein coding sequence.
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30-AUG-2001; 2001US-315768P.
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P-PSDB; AAO18661.
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1 ATGITGGGTAAGGICAICGAIACCCITACAIGCGGCTICGCCGACCICGIGGGGTACAII

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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCW)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV The recombinant HCV B1 and/or B2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACCTCTGCGGGATCTGTTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant E1, E2, and E1/E2 proteins. The recombinant E1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage in a serving of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV mare amitibodies in a sample, and in a servicyping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated
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                                                                                                                                                 CTCGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTTGATTGTGATGCTACTTT 783
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                                                                                                                                                                                                                                                                                                                                        HCV; E1, E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                                                                                        CGGATCCCACAGAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGCGGGT
                              GAGACGGTGCAGTGCTAGTTGCTCAATCTTATCCCGGCCATAACGGGTCACCGTATG
                                        Purifying recombinant hepatitis C virus (HCV) B1 and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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into a reversed phase hybridisation assay for determining the presence the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known
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                                                                                                         Score 778.8; DB 17; Length 2086; Pred. No. 1.2e-199; 0; Mismatches 2; Indels 0;
                                                                                    Sequence 2086 BP; 366 A; 635 C; 601 G; 484 T; 0 other;
                                                                                                               98.0%; initarity 99.7%; Conservative 0
                                                                                                                              Best Local Similarity
Matches 780; Conserv
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TIGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC 594
                                                                                                                                ATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGAGAACAACTCTTCCCGCTGC
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30-AUG-2001; 2001US-315768P.
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P-PSDB; AA018679.
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and E2 protein coding sequence constructs. These sequences are included
in vectors for the production of recombinant E1, E2, and E1/E2 proteins.
The recombinant proteins can then be isolated using a method of the
invention. In the method, the envelope proteins are purified by
carrying out a disulphide bond cleavage, or a reduction step with a
disulphide bond cleavage agent, after 19sis of recombinant host cells.
The constructs containing the purified HCV envelope proteins can be used
for vaccinating humans against HCV, for in vitro detection of HCV
constructs can also be immobilised on a solid substrate and incorporated
into a reversed phase hybridisation assay for determining the presence or
the genotype of HCV The new purification method preserves the
conformation of the recombinantly expressed E1, E2 and E1/E2, and
eliminates contaminating proteins. Antigens isolated using this method
are more reactive with human sera than those isolated by known
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                                                                                                                    HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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Pred. No. 1.2e-199;
0; Mismatches 2;
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Matches 780; Conservative
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                                                                                    The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HV single or specific oligomeric recombinant envelope proteins selected from an E1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans vaccines or therapeutics, in HCV SI and/or E2 proteins are useful as vaccines or therapeutics, in the preparation of medicament, and for tests, for raising antibodies, in the preparation of medicament, and for treatment of patients suffering from HCV Infection. The present sequence is a coding sequence described in the exemplification of the invention.
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New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                    DB 24; Length 2434;
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                                                                                                                                                                                                                                                           Sequence 2434 BP; 434 A; 745 C; 714 G; 541 T; 0 other;
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                                                                                                                                                                                                                                                                                      96.6%; Score 767.8; DB 24
99.6%; Pred. No. 1.1e-196;
Live 0; Mismatches 2;
                                                                    Example 2; Page 212-215; 243pp; English.
                                                                                                                                                                                                                                                                                                        Best Local Simiario,
Matches 780; Conservative
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Best Local Similarity
                                              from HCV infection
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The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) CC internal ribosome entry site (IRES) region coding for one or more NS3, conternal ribosome entry site (IRES) region coding for one or more NS3, CC internal ribosome entry site (IRES) respectively. The location of the materions are detailed in the specification. Also included are CC washing a recomprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an expense on the altered nucleic acids, (3) a recombinant cell human hepatoma cell comprising the altered nucleic acids (3) a recombinant cell produced by introducing control a human hepatoma cell the altered nucleic acids (4) producing an into a human hepatoma cell the altered nucleic acids (4) producing an control control HCV replicon enhanced cells made in the control of method; and (6) measuring the ability of a compound to affect HCV method; and (6) measuring the ability of a compound to modulate one or more HCV interactions, producing HCV RNA and proteins, and providing a system interactions, producing HCV RNA and proteins, and providing a system interactions the ability of a compound to modulate one or more HCV
                                                               1075 CCTCGCCTACTATCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTT 1134
CCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCCATTGGGGAGTCCTGGCGGG 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HC NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /_________HCV polyprotein"
/product = "The polyprotein consists of the Core, E1,
fnote= "The polyprotein consists of the Core, E1,
E2, P7, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins"
                                                                                                                                                                                                                                                                                                                                                                                 HCV; ds; Con 1; adaptive mutation; liver failure; cirrhosis; hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV; internal ribosome entry site; IRES; NS5A; HCV replication.
                                        TCTCGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTTGATGTGATGCTACTCTT
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P-PSDB; ABG32451.
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                                                                                                                                                                                  Gaps
activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular car The present sequence is the HCV replicon Con 1, used as a basis
                                                                                                                                         Length 9605;
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                                                                                                 Sequence 9605 BP; 1910 A; 2883 C; 2733 G; 2079 T; 0 other;
                                                                                                                                                                                49; Indels
                                                                                                                                       Score 703.6; DB 24;
Pred. No. 3.4e-179;
0; Mismatches 49;
                                                            adaptive mutations of the invention.
                                                                                                                                       Query Match
Best Local Similarity 93.7%;
Matches 733; Conservative
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New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication
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                                                                                                                                                                                                                                                             /*tag= a //trag= nHCV polyprotein" //trag= "HCV polyprotein" //product= "The polyprotein consists of the Core, E1, - //note= "The polyprotein consists of the Core, E1, - replace (3625,G) /*tag= b /*tag= b
                                              HCV; ds; Con 1; adaptive mutation; liver failure; cirrhosis; hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV; internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e: The present sequence is not shown in the specification but created by the indexer using the HCV sequence appearing as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 88.5%; Score 703.6; DB 24; Length 9605; Best Local Similarity 93.7%; Pred. No. 3.4e-179; Matches 733; Conservative 0; Mismatches 49; Indels 0;
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Hepatitis C virus Con 1 isolate DNA mutant 1.
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                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                            Hepatitis C virus.
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                                                                                                                                                                    Synthetic.
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Gaps

4 TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATTCCG 63

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ABK91424 standard; DNA; 9605 BP.

ABK9142 RESULT

ABK91424;

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The invention relates to nucleic acid molecules comprising altered HCV (CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, internal ribosome entry site (IRES) region coding for one or more NS3, cor EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are mutations are detailed in the specification. Also included are comparable acids, which is transcriptionally coupled to an the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell buman hepatoma cell comprising control and nucleic acids; (3) a recombinant cell produced by introducing the altered nucleic acids; (3) a recombinant cell produced by introducing an into a human hepatoma cell the altered nucleic acids; (4) producing an expression and expression enhanced cells made in the containing at a therefore a billity of a compound to affect HCV method; and (6) measuring the ability of a compound to affect HCV containing HCV Raplicons and HCV replicon enhanced cells are useful in studying HCV replication and expression, and HCV and host cell cut accover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated was liver failure, cirrhosis and hepatocolellular carcinoma. The present sequence is an HCV replicon on 1 mutant of the invention.

CC ABK91411 and the indexer using the HCV sequence appearing as
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                                                                           /note= "The polyprotein consists of the Core, El, E2, P7, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins" /*tag= b
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93.7%; Pred. No. 3.4e-179;
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                                                                 /product= "HCV polyprotein"
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HCV; ds; Con 1; adaptive mutation; liver failure; cirrhosis; hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV; internal ribosome entry site; IRES; NSSA; HCV replication; mutant. /note= "The polyprotein consists of the Core, El, E2, P7, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins" replace (4380,G) Hepatitis C virus Con 1 isolate DNA mutant 3. Location/Qualifiers 342..9374 /*tag= a /product= "HCV polyprotein" BP. ABK91426 standard; DNA; 9605 (first entry) Hepatitis C virus. Synthetic. 15-NOV-2002 ABK91426; RESULT 10 ABK91426

/*tag=

mutation

WO200259321-A2

01-AUG-2002

ATGATCATGCATACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCCTCCCGCTGC 1055 815 875 243 935 303 GGAGTGTACCATGTCACGAACGACTGCTCCAACGCAAGCATTGTGTATGAGGCAGCGGAC 995 363 755 123 124 GAGGACGCCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTC 183 364 TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACCACAATA 423 63 696 TTGGGTPAGGTCATCGTACCTCACGTGCGGCTTCGCCGATCTCATGGGGTACATTCCG TIGETITICATE TO THE TOTAL CONTROL OF THE TOTAL OF THE TOTA 244 GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC 304 ATGAICATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGCTGC CTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG TTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGGTACATTCCG Gaps 1 88.5%; Score 703.6; DB 24; Length 9605; Similarity 93.7%; Pred. No. 3.4e-179; . Sequence 9605 BP; 1911 A; 2883 C; 2732 G; 2079 T; 0 other; Indels 49; 0; Mismatches Conservative Query Match Best Local Simil Matches 733; C 4 64 95/ 816 184 876 936 용 ð g g g ò 셤 ò ઠે 음 ઠે ò ò

The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) respon coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mexpression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an expression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an expression acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an CHCV (hepatitis C virus) replicon enhanced cells caids; (4) producing an CHCV (hepatitis C virus) replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replicons and HCV and host cell cativity. The HCV replicons and expression, and providing a system of interactions, producing HCV RAM and proteins, and providing a system of interactions producing HCV RAM and proteins.

Continue activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activity activities e.g. to discover drugs which may treat HCV mediated activity activities e.g. to discover drugs which may treat HCV mediated activity activities e.g. to discover drugs which may treat HCV mediated activity act ABK91411 and the information in Claim 9.

New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication

Claim 9; Page -; 69pp; English.

and expression

(RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI

16-JAN-2002; 2002WO-EP00526. 23-JAN-2001; 2001US-263479P. ö

Paonessa

Migliaccio G,

WPI; 2002-599793/64. De Francesco R,

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The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, internal ribosome entry site (IRES) region coding for one or more NS3, care to the altered nucleic acids, which is transcriptionally coupled to matered nucleic acids, which is transcriptionally coupled to more altered nucleic acids, (3) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an into a human hepatoma cell the altered nucleic acids; (3) an HCV replicon enhanced cells made in the functional HCV replicons and HCV replicon enhanced cells are useful in studying HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and expression, and HCV and host cell studying HCV replication and expression, and PCV and host cell studying HCV replication and expression, and PCV and host cell activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities actuence appearing as the present sequence is not shown in the specification but the information in Claim 9.

Note: The present sequence is not shown in the specification but we was created by the information in Claim 9.
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NSS encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRBS) region, useful in studying HCV replication and expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9605 BP; 1909 A; 2884 C; 2733 G; 2079 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 88.5%; Score 703.6; DB 24 Local Similarity 93.7%; Pred. No. 3.4e-179; Les 733; Conservative 0; Mismatches 49;
                                                                      Claim 9; Page -; 69pp; English.
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/protein: "HCV polyprotein"
/protein: "The polyprotein consists of the Core, El,
Horden "The polyprotein consists of the Core, El,
E2, P7, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins"
replace (6463,A)
/*tag= b
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                                                                                 484 GACCICIGGGGATCIGICTICCICGICTCCCAGCIGITCACCAICTGGCCIGGCAI
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the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replicons and HCV replicon enhanced cells are useful in interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities as liver failure, cirrhosis and hepatoceallular carcinoma. The present sequence is an HCV replicon Con 1 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV sequence appearing as
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0; Mismatches 49;
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93.7%; Pred. No. 3.4
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Matches 733; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification, Also included are (1) an expression vector comprising a nucleotide sequence coding for
                              GAGACAGTACAGGACTGCAATTGCTCAATATATCCCGGCCACGTGACAGGTCACCGTATG
                                                                                                 GCTTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGGTATCGCAGTTACTC
                                                                                                                                                  CGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCCCATTGGGGAGTCCTGGCGGGT
                                                                                                                                                                                                                          CTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGATTGTGATGCTACTTTT
                                                                     GCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
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hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
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New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication and expression
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/product= "HCV polyprotein"
/note= "The polyprotein consists of the Core, El,
/note= "The polyprotein consists of the Core, El,
race, Ty, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins"
replace (6911,C)
/*tag= b
                                                                                                                                                                                                                                                                 HCV; ds; Con 1; adaptive mutation; liver failure; cirrhosis; hepatocellular carchnoma; NS3; NS5; encephalomyocarditis virus; EMCV; internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
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342..9374
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diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV replicon Con 1 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV sequence appearing as ABK91411 and the information in Claim 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGATGTACCATGTCACGACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
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                                                                                                                                 DB 24; Length 9605;
                                                                                                 Sequence 9605 BP; 1910 A; 2882 C; 2733 G; 2080 T; 0 other;
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                                                                                                                               Score 703.6; DB 24
Pred. No. 3.4e-179;
0; Mismatches 49;
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Best Local Similarity 93.7%;
Matches 733; Conservative (
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Location/Qualifiers 342..9374 /*tag= a

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Hepatitis C virus Con 1 isolate DNA mutant 8.
                                                                                                                                    Claim 9; Page -; 69pp; English.
                                                                                                       Francesco R, Migliaccio G,
                                                                                    16-JAN-2002; 2002WO-EP00526
                                                                                          23-JAN-2001; 2001US-263479P
      15-NOV-2002 (first entry)
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                               Hepatitis C virus.
Synthetic.
                                                                       WO200259321-A2
                                                             mutation
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the information in Claim 9.

using

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1056 TGGGTAGCGCTCACTCCCACGCTCGCGCCAGGAACGCTAGCGTCCCCACTACGACGATA 1115
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TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATTCCG
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The present sequence is an thought on modulate one or more HCV was created by the indexe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "HCV polyprotein"
/note= "The polyprotein consists of the Core, E1,
E2, P7, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins"
/*tag= b
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                                                                                                                                                     HCV; ds; Con 1; adaptive mutation; liver failure; cirrhosis; hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
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88.5%; Score 703.6; DB 24;
Best Local Similarity 93.7%; Pred. No. 3.4e-179;
Matches 733; Conservative 0; Mismatches 49;
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The invention relates to nucleic acid molecules comprising altered HCV (C) NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, conternal ribosome entry site (IRES) region coding for one or more NS3, context of the specification. Also included are mutations are detailed in the specification. Also included are cutations are detailed in the specification. Also included are context on the specification and so the specification and so the altered nucleic acids, which is transcriptionally coupled to a cyogenous promoter; (2) a recombinant cell produced by introducing the altered nucleic acids; (3) a recombinant cell produced by introducing context and entry replicon and electrication enhanced cells made in the functional HCV replicon enhanced cells made in the continuity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and expression, and HCV and host cell studying HCV replication and expression, and HCV and host cell studying Hc ability of a compound to modulate one or more HCV contexties e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated by the indexer using the HCV sequence appearing as a greated by the information in Claim 9.
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                                                                                             /note= "The polyprotein consists of the Core, E1, E2, P7, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins" replace (6936,G) /*tag= b
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              Location/Qualifiers
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| 0 00 0 0 0 0000 0 00 HHHHHHHHHHHHMMMMMMMMMM | RESULT 1 AV755731/C LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISN TITLE JOURNAL COMMENT FEATURES |
| <pre>te version 5.1.6 sw model sw model 18:03:34 ; Search time 2045.18 Seconds (without alignments) 9447.586 Million cell updates/sec CGATACTCTTTGCTCCCTAATAG 795 : 1.0 i2238056 residues isen parameters: 45562784 immaries</pre> | results predicted by chance to have a to the score of the result being printed, of the total score distribution. SUMMARIES ID AV755731 AV755731 AV758366 BX35664 BX35664 AL053013 Drosophil |
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organism="Homo sapiens"

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/mol type="mRNA"
/do xref="teaxon:966"
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/clone=Tib="team obna was primed with a NotI-oligo(dT)
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primer. Five prime end enriched, double-strand cDNA was
primer. Five prime and enriched, double-strand cDNA was
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BX335664 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CS0DI015YB03 3-PRIME, mRNA sequence.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invirrogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InvirroGen Corporation 1600
http://fulllength.invitroges.com/ InvirroGen Corporation
Location/Qualifiers
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                  /tissue_type="Bone marrow" /cell_type="CD34+ hematopoietic stem/progenitor cell" /lab host="BM25.8" /clone lib="BM25.8" /clone lib="BM" priplEx2; Site_1: sfilA; Site_2: sfilB" /note="Voctor: priplEx2; Site_1: sfilA; Site_2: sfilA; Site_2: sfilA; Site_2: sfilA; Site_2: sfilA; Site_3: sfilA; 
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clone="BMFAKA03"
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Homo sapiens
                                                                                                                                                                                                                                                      tch 11.5%;
al Similarity 60.9%;
184; Conservative
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1 (bases 1 to 492)

1 (bases 1 to 492)

2 (J. Zhao, M., Hung, O., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H., Gu, Y., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, Gu, Y., Li, N., Qian, B., Liu, F., Yu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gao, G., Wang, Z., Zhang, Q., Chen, S., Han, Z. and Chen, Z. Homo sapiens cDNA BM clones
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801991 (ex.45)
                                                                                                                                                                                                                                                                        r: pTriplEx2; Site_1: sfiIA, Site_2: sfiIB"
137 g 97 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAAT
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                                       /organism="Homo sapiens"
/mol type="mRNA"
/db xref="texon:960"
/clone="BMFAKB03"
/tissue type="BMFAKB03"
/cell type="EMZ5.8"
/lab host="EMZ5.8"
/clone lib="BMS5.8"
/note="Vector: pTriplEx2; Site_1: sfilA, Site_2: sfilE
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This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             Score 115.6; DB 9;
pred, No. 6.4e-19;
0; Mismatches 109;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Geoggawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                           SCSCTSSBSTISSTBSMISSSBTCTSSSSSSBTTSSTTTSTKSSBTTTSBTBSSSST 844
                                                                                                                                                                                                                                                                                                                                                                 203 TGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCCGGGATGTACCATGTCACGA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGCGTGCCCTGCGTTCGGGAGACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                         263 ACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCCG 322
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                                                                                                                                                                                  vector. Library was normalized.
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                                                                                                              Gaps
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebnydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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                                                                          Length 1201;
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aa26bli.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814365 5',
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                BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
The library is named RPCI-98 and was constructed by partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 GCGTTCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCCACGCTCGCAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 TTTTTSSGSGYGKGCSSGSBSCSCCSSCSCSSSSCCCCCCCCSCSSYCCSSBSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            575 ATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA
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                                                                                                                                                                                                                                                                                                                                                                                            511 others
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/organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 16.1%; Pred. No. 2.1; ies 70; Conservative 166; Mismatches 196;
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6.1%; Pred. No. 2.
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9
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905 KSSSSGSVSSGSGSGS 920
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Azabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
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F13A13-Sp6 IGF Arabidopsis thaliana genomic clone F13A13, genomic
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4924.f For more information about this cluster, see http://www.genoscope.cns.fr/
                                                                     cgi-bin/dluster.cgi?seq=CL0BA006ZG08RPl&cluster=4924.f. Contact cgi-bin/dluster.cgi?seq=CL0BA006ZG08RPl&cluster=4924.f. Contact Fang Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CL0BA006ZG08RPl. Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1012 GKKKTTTTWMMAAATWTHTTWTTTYTCTAAWGGGTAKCVAKCCCMCCCCCAMGCTS
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/clone="ludge:844365"
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/lab_host="bhl08"
/clone lib="NcI_CGAP_GCBI"
/clone lib="louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was primed with a NcI I - Oligo dCI) primer
/clone-grand cDNA was ligated to Eco RI adaptors
/constructed by Bento Soares and M. Fatima Bonaldo."
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5-PRIME, mRNA sequence.
AL513886
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Upublished
On Feb 13, 2001 this sequence version replaced gi:12777380.

Contact: Genoscope
Contact: Mational de Sequencage
Benoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 382.
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/db_xref="GDB:6032522"
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Chlamydomonas rainhardtii
Eukaryota, Viridiplantes; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="IGF"
//ote="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
1 541 c 178 g 404 t 11 others
                                                                                                                                                  Dept. of Biology, University of Pennsylvania, Philadelphia, PA 19104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
A large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433
non-redundant expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1195)
Peng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P.,
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Pred. No. 8.2;
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                                                                                                                                                                                                                                                                                                                                 organism="Arabidopsis thaliana"
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                                                                                                                                                                                                      Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
Seg primer: Sp6
                                                                                        Other GSSs: F13A13-T7
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic_DNA"
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/db_xref="taxon:3702"
/clone="F13A13"
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High quality sequence stop: 98.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              /sex="hermaphrodite"
                                                                                                                                           University of Pennsylvania
                                               Ecker,J.
BAC End Sequences at ATGC
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                                                                                                                                                                                       Tel: 215-898-9384
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                                                         TITLE
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AV392165 AV392165 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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| organism="Chlamydomonas reinhardtii" |
| mol_type="mRNA" |
| strain="C9" |
| db_xref="taxon:3055" |
| clone="CM096g04_r" |
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| dev_stage="photoautotrophic growth" |
| clone lib="Chlamydomonas reinhardtii C9" |
| clone lib="Chlamydomonas reinhardtii C9" |
| clone lib="Chlamydomonas reinhardtii C9" |
| clone lib="Wettor: pBluescriptII SK-; Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 CCGCAAGGTGTTTGACGAGATCAAGGAGTACGTGCTGAACCTCAAGGCCCAGAACCCCAG
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Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. A large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardii. I. Generation of 3433 non-redundant expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
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Pred. No. 8.2;
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The First Laboratory for Plant Gene Research
Kararaa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 179;
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290 CTTCGCCGTCGCTGCGTGGGCCACTCGCTGGCGGCGCCGCCGCCGGCTGCCTGTCGAT 349
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Chlamydomonadaceae; Chlamydomonae.
1 (bases 1 to 584)
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1031095C12.yl C. reinhardtii CC-1690, Stress II (normalized)
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Pred. No. 9.1;
0; Mismatches 179; Indels 0
mol_type="mRNA"
gtrain="CC-1690 wild type mt+ 21gr"
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1031037A07.y2 C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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                                                                                  1. .551
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/dev_ge="photoautotrophic growth"
/clone lib="Chlamydomonas reinhardtii C9"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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45.3%; Pred. No. 9.1;
tive 0; Mismatches 179; Indels
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Location/Qualifiers
1. .552
                                   Email: ynakamu@kazusa.or.jp,
Location/Qualifiers
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DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
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Lefebvre

linear EST 19-SEP-2001

(normalized),

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Gaps

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/note="Vector: pBluescript II SK-; Site_I: EcoRI; Site_2:
Xho1; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAPP (accetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA,
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRN (5') and Xhol (3') sites,
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
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534 bp mRNA linear EST 09-MAY-2003 psH8036xB09f_300663 psHB: Infected hypocotyl soybean host. 48 hrs post infection Phytophthora sojae cDNA clone sHB036B09 5, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 GCÁCCGCTTCAACAÁCCCCACCGTGCTGAATTCGCCCCCACAAGTACCTGCTGTCCAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 CGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCC 380
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    .525
/organism="Chlamydomonas reinhardtii"

                   Chlamydomonadaceae; Chlamydomonas.
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DCMB Box 3100
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 CAACATGCGCACCCTGCTGCTCAC 306
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894043G08.yl C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone lib="C. reinhardtii CC-1690, Stress II (normalized
, Lambda Zap II"
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Chlamydomonas reinhardtii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3055"
/clone lib="C roll-
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                          Email: chauser@duke.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:9210174
                                                                                                                       Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
DCMB Box 91000
Duke University
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/mol_type="mRNA"
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                            1 (bases 1 to 671)
Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvo Grossman,A., Chang,C.-W., Silflow,C. and Stern,D.,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              533 egecelaceleceleceleses and control de co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Exist otherseraduke.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                              Vascular Plants. Project: 1031
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                                                                                                                                                                                                                                                                                                                                       Unpublished
Contact: Charles Hauser
DCMB Box 91000
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                                                                                                                                                                                                                          (bases 1 to 534)
Tyler, B.M., Judelson, H.S., Gijzen, M., Dean, R.A. and Waugh, M.E.
USDA-IFAFS: Expression of Phytophthora sojae genes during infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="sHB036B09"
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/clone_lib="psHB: Infected hypocotyl soybean host. 48 hrs
post infection"
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1031067F08.yl C. reinhardtii CC-1690, Stress II (normalized)
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                 Phytophthora sojae
Phytophthora sojae
Bukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae;
Phytophthora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1880 Pratt Dr., Blacksburg, VA 24061, USA
1821: 540-231-7318
Email: bmtyler@vt.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Phytophthora sojae"
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Location/Qualifiers
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Unpublished
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us-09-899-303a-5.rst

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthatroideae; Oryzae; Oryza.

1 (bases 1 to 608)
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Rudran, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="textorn:=9947"
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                                                                                                                                                                                                                                                                                                        Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
B5721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
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BACKWARD: aat taa ccc tca cta aag gg
Plate: 13 row: E column: 06
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Location/Qualifiers
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357 CCGCTGCTGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCAC 416 0; Gaps DB 14; Length 608; Score 39.8; DB 14; Length ered. No. 15; 0; Mismatches 92; Indels Query Match 5.0%; Best Local Similarity 50.8%; Matches 95; Conservative g

417 GACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTA 476 343 cerresceses de cerces de consecuencia de c 283 GGTAGTAGTACCGCCGCCAAAGTTGTTGTCGTCGAGGACGTGTTGGCCGCCGCCGCAGCG 224

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477 CGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCG 536 223 GGTACGGGCCTCCGCGGGGGCGTCGACGACGAGCCCGGGAGGCGCGAACTCCTGCTGCG 164 a a ò

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Search completed: December 20, 2003, 06:54:39 Job time : 2050.18 secs

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December 19, 2003, 16:55:48; Search time 1828.77 Seconds (without alignments) 10804.703 Million cell updates/sec
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1 AIGCCCGGTIGCTCTTICTC.....TGATGAACTGGTCCTAATAG 483
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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                                                     OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | A48671 Sequence 9 AR157327 Sequence AX452758 Sequence | AX685010 Sequence | A48673 Sequence 11 | AX452760 Sequence | AX685012 Sequence AF207766 Hepatitis | D00832 Hepatitis C | E04280 CDNA effection E04805 CDNA to 5'- | E07391 cDNA encodi | AR027786 Sequence | AR027783 Sequence AF054250 Hepatitis | AF054257 Hepatitis | Arusassa Hepatitis AF054255 Hepatitis | AF054254 Hepatitis | AF165052 Hepatitis D10750 Hepatitis C | AR119832 Sequence | AF054247 Hepatitis AF054249 Hepatitis | AR119833 Sequence | E04085 gDNA encodi D28929 Hepatitis C | AF054251 Hepatitis | AF054252 Hepatitis | D50481 Hepatitis C | AB049093 Hepatitis | M74900 Hepatitis | M74807 Hepatitis C | AB008446 Hepatitis | AF054255 neparitis AF054256 Hepatitis | AF483269 Hepatitis | Ariosusa hepacicis AF165051 Hepatitis | E04089 gDNA encodi D00574 Hepatitis C | | linear PAT 07-MAR-1997 | | Buyse,M. PROTEINS FOR DIAGNOSTIC AND | |
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| SUMMARIES | B ID | 6 A48671 6 AR157327 6 AX452758 | AX68501 | A48673 AR15732 | 6 AX452760 | AX685012 4 AF20776 | 4 HPC5TR | | E07391 | AR02778 | 6 AR027783 14 AF054250 | 4 AF0542 | 4 AF0542 4 AF0542 | 4 AF0542 | 4 AF1650 4 HPCJ49 | AR11983 | 4 AF0542 | AR11983 | _ 4 | 4 | 14 AF054252 | r 🕁 | ₩, | | 4. | 4. | r 🕶 | 4. | * 4 | 4 | ALIGNMENTS | 483 bp DNA tent WO9604385. 84 | | F., De, M.G. and VIRUS ENVELOPE | -A 9 15-FEB-1996; |
| d | Query Match Length D | 100.0 483 100.0 483 100.0 483 | 100.0 483 | 98.2 480 | 98.2 480 | 98.2 480 | 90.1 1880 | 90.1 2540 | 90.1 2540 | 89.7 1539 | 89.7 1863 89.6 9580 | 89.4 8780 | 89.4 8780 | 89.1 8781 | 89.1 9379 | 89.1 9595 | 89.1 9595 | 89.1 9599 | 88.7 577 88.7 618 | 88.7 8779 | 88.7 8780 | 88.7 9410 | 88.7 9435 | 88.7 7595 | 88.4 1635 | 88.4 3296 | 88.4 8781 | 88.4 9361 | 88.4 9379 | 88.1 577 '88.1 1413 | | 8671 quence 9 from Pa 8671 8671.1 GI:23023 | unidentified unidentified unclassified | D 48 Bosm TITI SE | rent: WO 9604385 |
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Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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purified hepatitis C virus envelope proteins for diagnostic and
therapeutic use
patent: US 6245503-A 9 12-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCC
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/db_xref="taxon:11103"
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Other publication CA 2172273 960215
Other publication AU 3382495 960304.
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Macrens, G., Bosman, F., De, M.G. and Buyse, M.
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PALCHT: WO 9604385-A 11 15-FBB-1996;
INNOGENETICS NV (BE)
Other publication CA 2172273 960215
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Viruses; ssRNA positive-strand viruses, no
Hepacivirus.
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100.0%; Score 483; DB 6; L
Best Local Similarity 100.0%; Pred. No. 3.1e-113;
Matches 483; Conservative 0; Mismatches 0;
'note="unnamed protein product"
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Patent: WO 02055548-A 9 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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/product="unnamed"
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/codon_start=1
/protein_id="CAD38070.1"
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                        Gaps
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                                              Length 480;
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                                                 DB 6;
                                                Score 474.2; DB 6;
Pred. No. 5.7e-111;
0; Mismatches 3;

    .480
    /organism="Hepatitis C virus"
/mol_type="genomic DNA"
/db_xref="taxon:11103"

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Sequence 11 from Patent EP1211315.
AX452760 AX452760.1 GI:21712445
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/product="unnamed"
149 c 123 g
/organism="unknown"
149 c 123 g
                                                  Query Match
Best Local Similarity 99.4%;
Matches 476; Conservative
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                                              /organism="unidentified"
/mol type="genomic DNA"
/db_xref="taxon:32644"

1. -477
/note="unnamed protein product"
/codon start=1
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1 (bases 1 to 480)

1 (bases 1 to 480)

Wastens, G., Bosman,F., De Martynoff,G. and Buyse,M.-A.

Purified hepatitis C virus envelope proteins for diagnostic and
therapeutic use
Patent: US G45503-A 11 12-UUN-2001;
LOGALION/Qualifiers
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Pred. No. 5.7e-111;
0; Mismatches 3;
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Sequence 11 from patent US 6245503.
ARI57328
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               publication AU 3382495 960304
Location/Qualifiers
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/product="unnamed"
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Sato, C.
Characteristics of hepatitis C viral genome associated with disease
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Hepacivirus.
1 (bases 1 to 9379)
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Nagayama, K., Kurosaki, M., Enomoto, N., Miyasaka, Y., Marumo, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /noTe="isolated from a patient with liver cirrhosis and hepatocellular carcinoma (HCC-5)"
                                                                                      Direct Submission
Submitted (23-NOV-1999) Second Department of Internal Medicine,
Tokyo Medical and Dental University, 1-5-45 Yushima Bunkyo-ku,
                                                                                                                            181 TGCGTTCGGGAGGCCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACCCCTGGGCC
                                                                                                                                                                                                                                                                                                                     241 AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT
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2 (bases 1 to 9379)
Nagayama,K., Kurosaki,M., Enomoto,N., Miyasaka,Y., Izumi,N.
                 Length 480;
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Hepatitis C virus strain MD25 complete genome.
AF207766
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                Score 474.2; DB 6;
Pred. No. 5.7e-111;
0; Mismatches 3;
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Location/Qualifiers
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ilarity 99.4%;
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Hepatitis C virus
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/codon_start=1
/protein_id="CDAB6523.1"
/db_xref="G1:29371418"
/db_xref="G1:29371418"
/xranlala.ton="MSGCSFSTFLLALLSCLTIPASAYEVRNVSGVYHVTNDCSNSSI
VYEAADMINHTPGCYCVREGASRGWVALFPFLAARASVPTTTRRHYDLJVGAAA
FCSAMYVGDLCGSVFLVSQLFTFSPRRHQTVQDCNCSIYPGHVSGHRMAWDMMANNWA
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Viruses; BSRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Purified Hepatitis C Virus envelope proteins for diagnostic and
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                         Score 474.2; DB 6;
Pred. No. 5.7e-111;
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/mol type="genomic DNA"
/db_xref="taxon:11103"
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Patent: WO 02055548-A 11 18-JUL-2002;
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Location/Qualifiers
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'49 c 123 g
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/ (Ab. Xref="0.1") 176: 708.03.03.07

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ö 121 0; Gaps Ouery Match 90.7%; Score 438.2; DB 14; Length 9379; Best Local Similarity 95.2%; Pred. No. 1e-101; Matches 452; Conservative 0; Mismatches 23; Indels 0; 1955 t 2719 9 GIYLLPNR" 1 2852 C 1853 62 BASE COUNT ORIGIN g g 8 ò ઠે

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Okamoro, H., Okada, S., Sugiyama, Y., Kurai, K., Iizuka, H., Machida, A., Miyakawa, Y. and Mayumi, M.

Nucleotide sequence of the genomic RNA of hepatitis C virus isolated from a human carrier: comparison with reported isolates for conserved and divergent regions
J. Gen. Virol. 72 (Pt 11), 2697-2704 (1991)
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Hepatitis C virus gene for structural protein, partial cds,
isolate:HC-J4.
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Hepacivirus.
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                               Hotta, H., Doi, H., Hayashi, T., Purwanta, M., Soemarto, W., Mizokami, M., Obba, K. and Homma, M. Analysis of the core and El envelope region sequences of a novel variant of hepatitis C virus obtained in Indonesia Arch. Virol. 136 (1-2), 53-62 (1994)
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Kawachi-gun, Tochigi-ken 329-04
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S Okamoto, H and Nakamura, T.
HIGHLY SENSITIVE DEFFECTION METHOD OF NON-A NON-B TYPE HEPATITIS
HIGHLY SENSITIVE DEFFECTION PRIMER AND OLIGONUCLEOTIDE PRIMER
VIRUS USING OLIGONUCREOTIDE PRIMER AND OLIGONUCLEOTIDE PRIMER
D 1993023200-A 2 02-FEB-1993;
NAKAMURA TETSUO
PD 02-FEB-1993
PF 26-APR-1991 JP 1991191376
PR 12-CUN-1990 1P 90P 1991191376
PR 12-CUN-1990 1P 90P 1990 153402
PI CKAMOTO HIROAKI, NAKAMURA TETSUO
PC C12Q1/68,C12N15/51,C12Q1/70;
CC strandedness: Double;
CC topology: Linear;
CC hypochetical: No;
CC anti-sense: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E04805 2540 bp RNA linear PAT 29-SEP-1997 cDNA to 5'-terminal region of gRNA of Hepatitis nonA nonB virus. E04805 1 GI:2173001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG 301
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Pred. No. 6.6e-101;
0; Mismatches 25; Indels
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/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
a 776 c 741 g 553
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ilarity 94.7%;
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Matches 450; Conserv
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/ note="82 bp upstream of Styl site"
342. . . . . 1880
/ note="putative"
/ codon start=1
/ product="structural protein"
/ db xref="c1:21514"
/ translation="MSTNPREPRERANARQEYPWPLYCNEGLOWAGWILSPRG
SRESWOPTDPRRESRINGKUIDTLTGGFADIMGYIPLYGABLGGAARALABGRAUG
GVNATRANEGCSFSIFLIALLSCITIPARARASVETTIRRHUDLUGABAECSAMY
VGDLGGSVFUNGCSFSIFLALLSCITIPARARASVETTIRRHUDLUGABAECSAMY
VGDLGGSVFUNGCSFSIFLAGLAGATACHAGAAV
SQLIRIPQAVVDMVAGAHWGVLAGAAVGAGAYUTURALLSCAMY
SQLIRIPQAVVDMVAGAHWGVLAGAAVGAWHUNGVARANARANASCHERALSCAMA
SGLTSTLASLESGASORIQIVWTNGSWHINRTALNCNDSLHTGFLALLSTTHRFNS
GCPERRASCRPIDWFAQGWGPITYTEPDSPDQPRPYCWHYAPRPCGIVPASQVCGPVYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2540 bp RNA linear PAT 29-SEP-1997 of type non-A non-B hepatitis virus.
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                              /organism="Hepatitis C virus"
/mol type="genomic RNA"
/isolate="HC-J4"
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   cocation/Qualifiers
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CDNA encoding a part of
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E04260.1 GI:2172463
JP 1993023200-A/2.
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20-JUN 1991 JP 1991247120

CAMOTO HIROAKI, NAKAMUTA TETSUO

CIRNIS/SI, CIRNI/21, CI2P21/02, CI2Q1/70, G01N33/53, G01N33/569,

G01N33/576;
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BD7391.1 GI:2175530

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/note='Structural protein of chimpanzee
hepatitis non-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .2540
/organism='Hepatitis non-A non-B virus'.
/strain='HC-J4'
1. .341
ide 342. .1490
ide 7note-structural protein of chimpan hepatitis non-A non-B virus'
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                             E07391 2540 bp RNA linear Pl
CDNA encoding chimpanzee hepatitis non-A non-B virus.
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/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
a /776 741 g 553
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JP 1994125777-A/4
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hypothetical: No;
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2 Okamoto, H. and Nakamura, T.
Benerichon system FOR NON-A NON-B HEPATITIS VIRUS RELATING ANTIGEN
AND ANTIBODY, POLYNUELECTIDE AND POLYPEPTIDE
PATENT: JP 1993091884-A 2 16-APR-1993;
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342. .2540
/note='protein coded by Hepatitis nonA nonB
virus gene'.
Location/Qualifiers
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1167 ATCCCGGCCATTTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTC 1321
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Pred. No. 6.6e-101;
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/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
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SHTTSTLASLESPGASQRIQLVNTNGSWHINRTALNCNDSLHTGFLAALFYTHRENSS
GCPERMASCREIDWFAQSWGPITYTEDDSPDQRYCWHYAPRRCGIPPASQVCGPYC
PRESPVYVGTTBRGVPTTETDVMLLNTRPPQGNWFGCTWMSTGFTKTCGG
PPCNIGGYGNHTLTCPTDCFRKHPEATYTKCGSGPWIFPRCLVDYPYRLWHYPCTFNF
SIFKVRWYVGGVGHTLAGACNWTRGERCNLEDRDSSLISPLLISTTEWQILPCAFTTL
                                                                                                                          AGCTGTTCACCTTCTCGCCTCGCCGGGATGAGACAGTGCAGGACTGCAATCT 1266
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                       1147. CTGCTTTCTGCTCCGCTATGTACGTGGGGGATCTCTGCGGGATCTGTTTCTCTGCTCTCTGCCC 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C protein; E protein; E2 protein; NS1 protein; NS2 protein; NS3 protein; NS4 protein; NS5 protein. Hepatitis C virus Hepatitis C virus Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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GVRATRKTSERSQPRGWRQP1PKARRPEGRAWAQPGYPWPLYGNEGLGWAGWLLSPRG
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VGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHLASGHRMAWDMMMWSPTTALVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 9448)
Okamoto, H., Kojima, M., Okada, S., Yoshizawa, H., Iizuka, H.,
Tanaka, T., Muchmore, E.E., Peterson, D.A., Ito, Y. and Mishiro, S.
Genetic drift of hepatitis C virus during an 8.2-year infection in a chimpanzee: variability and stability
Virology 190 (2), 894-899 (1992)
                                                                                                   421
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Submitted (17-OCT-1991) Hiroaki Okamoto, Jichi Medical School, Immunology Division; Minamikawachi.machi, Kawachi-gun, Tochigi 29-04, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:0285-44-2111(ex:334), Fax:0285-44-1557)
Submitted (17-Oct-1991) to DDBJ by:
                                                                                              362 AGCTGTTCACCTTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT
                                                                                                                                                                                                                    1267 ATCCCGGCCATTTATCAGGTCACCGCATGGCTTGGGATATGATGATGATGAACTGGTC 1321
                                                                                                                                                                                          422 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTC 476
                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus genome, complete sequence. D13558 D01217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="polyprotein precursor"
/protein_id="BAA02756.1"
/db_xref="G1:221605"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic RNA"
/strain="HC-J4"
/isolate="HC-J4/83"
/db_xref="taxon:11103"
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Jichi Medical School
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302
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LLÍALPPRAYAMDREMAASCGGAVLVGLVFLTLSPYYKVFLTRLIWWLQYFTTRAEAH
MOWWPPLNYRGSRDAILLLTCAVNBELFDITKLLLAILGEMAUGAGTTRVPFVR
AQGIL RACKLVRKVAGGHYVQNAFKKLGALTGTYVKNHLTPLRDWAHAGLRDLAVAND
PVVFSDMETKVITWGADTAACGDIILGLPVSARRGKEIFLGPADSLEGQGWRLLAPIT
AXQQTRGALACGIITSLTRENROYQEGSVQVVSTATQSFLATCINGVCWYVHGAGSK
TLAGPKGPTTQMYTRVDLDIVGWQAPPGASSWTPCTCGSSDIYLVTRHADVIPYRRRG
DSRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVSRETT
                                                                                                                                                                                                                                                                                                                                                TDALMTGFTGDFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRG
RSGIYRRQTPGERPSGMPDSSVLCEVTQDAGCMSTELTPATSVRLRAXINTPGLAVCQ
BHLEFWESVPTGLSHIDAHELGGTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMYC
LIRLKPTLHGPTPLLYRLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLA
ALAAYCLTTGSSVIJGRILGSKPAVVPDREVLYGEPDEMBECASQLEYIEGGMQLAE
QFKQRALGLLQTATRGATAUVESKWRALETFWAKHWNFISGIQYLAGLSTLPGN
PAIASLLMAFTASITSPLTQNTLLFNILGGWVPAQLAPPSAAASAFVGAGIAGAAVGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLGKVLVDILAGYGAGVAGALVAFKVNSGEVPSTEDLVNLLPAILSPGALVVGVVCAA
ILRHVGPGEGAAVQMYNLL IAFASRGHHVSPTHYPPESDAARVTOLLSSLTTTOLLK
RLHGWINEDCSTPCSGASWLENDVWDM CTVLTDFKTWLQSKLLPRLPGVPPLSCORGY
GVWRGDGIMQTTCPCGAQIAGHVKNGSMRIVGPRTCSNTWHGTPPINAYTTGPCTPSP
ANDYSBALMWRYAEEFYDFYTGWTGPHYVTGWTTDNVKCPCYDAPBFFTSVDGYRLHR
YAPPCKPLIREDVAFQYGLNGYLGSQLPCBFPPDDVTVLTSWLTDPSHITAETAKRRL
ARGSPPSLASSSASQLSAPSLKATCTTHHDSPDADLIBANLLMRQEMGONITNVERC
                                                                                                                                                                                                                    MRSPVFTDNSSPPAVPOTFQVAHLHAPTGSGKSTKVPAAYAAQGYKVLVLNDSVAATL
GRAXMPKAHGIDPNIRTGARTITTGGPITYSGTYGKFLADGGCSGGSAVDIIICDBCHS
TDSTTILGTGTVLDDAETAGARLVVLATAPGSVTVPHPNIEDIGLSNNGEIPFYGK
AIPIEAIKGGRHLIPCHSKKKCDELAAKLTGLGLNAVAYYRGLDVSVIPPIEDIGNAVA
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ATALPDQASDDGDKGSDVESYSSMPPLEGEPGDPDLSDGSWSTVSEEASEDVVCCSMS
YTWTGALITPCAAEESKLPINPLSNSLLRHHNMYYATTSRSASLRQKKVTFDRLQVLD
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6005. .6104
/note="possible stem-loop structure in NS4 sequence"
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94.7%; Pred. No. 6.7e-101;
live 0; Mismatches 25;
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9413. .9448
/note="T-stretch of 36 bp"
nona c 2676 g 2045 '
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2529. .3359
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/product="NS2 protein"
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/product="C protein"
915. .1490
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1491. .2528
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                                                                 CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCCC 361
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                                          AGCIGITCACCTICTCACCTGGCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT 421
                                GCFITCGGAGGGAACTCCTCCCGTTGCTGGTGGCGCTCACTCCCACGCTCGCGGCCA 241
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Unknown.
Unknown.
Unclassified.
1 (bases 1 to 1539)
Okamoto, H. and Nakamura, T.
Oligonucleotide primers, and their application for high-fidelity
Oligonucleotide primers hepatitis virus
detection of non-A, non-B hepatitis virus
patent: US 5556458-A 17 05-JAN-1999;
Patent: US 5556458-A 17 05-JAN-1999;
Location/Qualifiers
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Pred. No. 1.7e-100;
0; Mismatches 26;
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US 5856458.
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Sequence 17 from patent
AR027786
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Best Local Similarity 94.5%;
Matches 449; Conservative 0
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HCV El construct P
                                                                                                                                         December 19, 2003, 16:53:58 ; Search time 133.529 Seconds (without alignments) 9764.351 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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NANB hepatitis vir NANBHV genomic fra AAQ24467 ABA03491 AAQ43889 AAQ63753 13 14 15

| Pragment of NANR h | , D | 모 | | | | 101 | cle 1 | Fragment of hepati | HCV J1 E domain co | HCV envelope regio | atitis Ĉ | 81 | us s | 18 (| is C | seq | #2 | Plasmid pidKE2 DNA | Fragment #6 isolat | on-B | v | Non-A, non-B hepat | v | NANB hepatitis vir | HCV El construct H | 8 C | Fragment #1 isolat | HCV envelope regio | Hepatitis C virus | Hepatitis C virus | Hepatitis C virus | HCV El construct H | Hepatitis C virus | ر ص | ıtit | Hepatitis C virus | |
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| AA015363 | AAQ29628 | AAX24843 | AAC86939 | AAF23492 | AAX24833 | AAQ35081. | ABA03492 | AAQ11076 | AAZ07647 | AAQ35085 | AAQ79750 | AAX26733 | AAX26728 | AAX00401 | AAQ79772 | AAX26739 | AAV60672 | AAL55222 | AAV60673 | AAQ64069 | AAT30387 | AAQ64068 | AAT30386 | AAQ27160 | AAT12704 | AAL48913 | AAV60668 | AAQ35086 | AAQ79758 | AAQ79759 | AAQ79760 | AAT12705 | AAL48914 | AAX00460 | 715 | . AAL48939 | |
| 12 | 13 | 20 | 22 | 22 | 20 | 14 | 13 | 12 | 20 | 14 | 16 | 20 | 20 | 50 | 16 | 20 | 19 | 25 | 19 | 15 | 16 | 15 | 16 | 13 | 11 | 24 | 13 | 14 | 16 | 16 | 16 | 11 | 24 | 20 | 13 | 24 | |
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| 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | | 43 | 44 | 45 | |

ALIGNMENTS

RESULT 1

HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera; Maertens G; Bosman F, Buyse M, De Martynoff G, AAT12707 standard; DNA; 483 BP. 95WO-EP03031 94EP-0870132 23-SEP-1996 (first entry) HCV El construct HCCI12A. (INNO-) INNOGENETICS NV. Hepatitis C virus 29-JUL-1994; 31-JUL-1995; WO9604385-A2 15-FEB-1996 AAT12707; AAT12707

Purifying recombinant hepatitis C virus (HCV) El and El envelope

WPI; 1996-129401/13

(first entry)

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AATI2704-T12709 and AATI2961-T12974 represent hepatitis C virus (HCV) E1 C and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins of the production of recombinant biles by the complex of the constructs. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage agent, after 1 psis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used to vaccinating humans against HCV, for in vitro detection of HCV or the constructs containing the purified HCV envelope proteins can be used to more sero-logical types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a selid substrate and incorporated the a genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated by known
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proteins – in presence of dissulphide bond cleavage agent, to
produce proteins suitable for direct use in vaccines or diagnostic
assays of HCV
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 483 BP; 85 A; 152 C; 123 G; 123 T; 0 other;
                                                                         21; 146pp; English.
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                                                                                Claim 23; Fig
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins elected from an B1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for the virco monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans from HCV infection
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                                                                                                                protein; E2 protein; infection; gene; vaccine; ds.
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                                                              Hepatitis C virus clone HCCI12A El protein coding sequence.
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100.0%; Pred. No. 2.6e-131;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 165-166; 243pp; English.
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Conservative 0
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30-AUG-2001; 2001US-315768P.
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                                                                                                                                  Hepatitis C virus; HCV; El virucide; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INNO-) INNOGENETICS NV.
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Matches 483; Conserv
                                                                                                                                                                                                                          Hepatitis C virus.
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AAL48916 standard; DNA; 483 BP.

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Matches 476; (
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and E2 protein coding sequence constructs. These sequences are included
in vectors for the production of recombinant E1, E2, and E1/E2 proteins.
The recombinant proteins can then be isolated using a method of the
invention. In the method, the envelope proteins are purified by
carrying out a disulphide bond cleavage, or a reduction step with a
disulphide bond cleavage, or a reduction step with a
classified by and cleavage agent, after 1ysis of recombinant host cells.
The constructs containing the purified HCV envelope proteins can be used
for vaccinating humans against HCV, for in vitro detection of HCV
constructs containing the purified HCV envelope proteins on ex-
more serological types of HCV present in a biological sample. The
constructs can also be immobilised on a solid substrate and incorporated
into a reversed phase hybridisation assay for determining the presence or
the genotype of HCV. The new purification method preserves the
conformation of the recombinantly expressed E1, E2 and E1/E2, and
climinates contaminating proteins. Antigens isolated using this method
are more reactive with human sera than those isolated by known
                                                            420
                                                                                                                                                                  TATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGATGTGGTCCTAA 480
                                                                                                                                                                                                   CAGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCTACTGCTAATC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                      CAGCTGTTCACCTTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purifying recombinant hepatitis C virus (HCV) E1 and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 23; Fig 21; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT12708 standard; DNA; 480 BP.
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Sequence 480 BP; 85 A; 149 C; 123 G; 123 T; 0 other;

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                                                                            ATGTCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCCCTGCTGTCTGATCTGACCATACCA
                                                                                                                       TGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans from HCV infection -
                                                          1 ATGCCCGGTTGCTCTTTCTCTTCTTCTTGGCCCTGCTGTCCTGTCTGACCATACCA
                               Gaps
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   Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus clone HCCI13A E1 protein coding sequence.
                               Indels
 Score 474.2; DB 17
Pred. No. 9.7e-129;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buyse M;
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Similarity 99.4%; 76; Conservative
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07-NOV-1991;
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                                        13-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCTGTTCACCTTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATC 420
                             The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligometic recombinant envelope proteins selected from an E1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for the view omitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                                                                                                                                                                          98.2%; Score 474.2; DB 24; Length 480; 99.4%; Pred. No. 9.7e-129; i.ve 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-B hepatitis virus; NANBHV; PCR; amplification
                                                                                                                                                                         Sequence 480 BP; 85 A; 149 C; 123 G; 123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase chain reaction; vaccine; antibody; ss.
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                Page 167-168; 243pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                  Query Match 98.2
Best Local Similarity 99.4
Matches 476; Conservative
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1147 CIGCITICIGCICCGCIAIGIACGIGGGGAICICIGCGGAICIGIIIICCICGICICCICC 1206 This sequence is the genome of the non-A, non-B hepatitis virus (NANBHV) strain HC-44. This sequence was derived by amplification by polymerase chain reaction. The nucleotide sequences derived from this amplification can be used to detect NANBHV infection which could not be detected by conventional methods. The detection kits allow highly specific and sensitive detection at an early phase of infection. The polypeptide product of this coding sequence can be used for the manufacture of vaccines and immunological pharmaceuticals and also to produce antibodies specific to NANBHV. gegricessasassechacicerecessariserissecissecessecrescesses CIGCITITCIGITIC CGCTATGIA CGTGGGGGATCT CTGCGGATCTGTTTTCCTTTCCC 362 AGCIGITCACCTICTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT 242 GGAACGCCAGGACCACCAACGACAATACGACGACGTCGATTTGCTCGTTGGGGGTG 967 ActicaAdcatricterArandadecaGcGaCarGarGarGcarActrccCGGGrGCGrGCCT 2 receeggrigerentreterreterretergecerrereterreterrande. ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGATGGTC 476 Gaps cDNA of NANBH virus strain HC-J5 and corresp. ö Length 1880; 25; Indels Sequence 1880 BP; 333 A; 593 C; 556 G; 398 T; 0 other; tch
al Similarity 94.7%; Pred. No. 4.7e-117;
450; Conservative 0; Mismatches 25; Disclosure; Page 11; 42pp; English 90JP-0304405 (IMMO) IMMUNO JAPAN INC Okamoto Recombinant cDNA of WPI; 1992-160959/20. Query Match Best Local Similarity Matches 450; Conserv P-PSDB; AAR24087 pharmaceuticals

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                                                                 866 AGCTGTTCACCTTCTCGCCTCGCCATGAGACAGTGCAGGACTGCAACTGCTCAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of NANB hepatitis virus polynucleotide N-2540-2 which codes for a non-A, non-B (NANB) hepatitis virus gene HC-OM. The polypeptide it encodes may be used in a system for detecting NANB hepatitis. This method is highly specific and sensitive, and can detect NANB hepatitis virus which could not be detected by
                                                                                                        422 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTC 476
                                                                                                                             Antigen related to non-A and non-B hepatitis virus - comprises non-translation region comprising 340 - 341 mols. of nucleotides, non-translation region comprising 1885 - 2551 mols. of nucleotides including region 1,149 and, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5' terminal of NANBH virus RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                 Non-A, non-B; virus; polymerase chain reaction; detection; sensitive; specific; HCV; NANBH; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 435; DB 14;
Pred. No. 5.2e-117;
0; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                           NANB hepatitis virus polynucleotide N-2540-2.
                                                                                                                                                                                                                                                    AAQ43889 standard; cDNA to mRNA; 2540 BP
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342..2540
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/*tag= b
/note= "from 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-A, non-B hepatitis virus.
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Best Local Similarity 94.7%;
Matches 450; Conservative
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90JP-0304405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NAKA/) NAKAMURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR38279.
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                                                                                                                                                                                                                                                                                                                                    21-OCT-1993
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                           362
                                                                                                                                                926
                                                                                                                                                                                                                                                                                            AAQ43889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAATGCCAGCGTCCCCACTACGACAATACGACGCCACGTCGACTTGCTCGTTGGGGGGG 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCTTTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCCC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCCCGGTTGCTTTCTTTTTTTTTTTTTTGCCCTGCTGTTCTTGTCTGACCATACCAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGTTCGGGAGGCCAACTCCTCCCGTTGCTGGGTGGCGCTCACCCCACGCTCGCGGCCA
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                                                                                                                                                #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to cuticle protein 1 and 2 secreting hepatitis C virus. The present sequence is a coding sequence provided in the exemplification of the invention.
                                                                                                                                            Cuticle protein 1 and 2 secreting hepatitis C virus related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cuticle protein 1 and 2 secreting hepatitis C virus (Japanese)
NoAbstract -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2187;
                                                                                                                                                                                    Cuticle protein 1; cuticle protein 2; hepatitis C virus; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 435; DB 19; Length 2
Pred. No. 4.9e-117;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2187 BP; 406 A; 669 C; 631 G; 481 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   /partial
/note= "no stop codon'
                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "AAM47264"
                                                                                                                                                                                                                                                                Location/Qualifiers
1..2187
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                         BP.
                       ABA03491 standard; DNA; 2187
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Best Local Similarity 94.7%;
Matches 450; Conservative
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                                                                                                        (first entry)
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P-PSDB; AAM47264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1996;
                                                                                                        15-MAR-2002
                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-0CT-1997
                                                               ABA03491;
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                                                                                                                                                                             The sequences given in AAQ63752-53 represent fragments of the non-A, non-B hepatitis virus (NANBHV) genome. These fragments were amplified using the primers given in AAQ63732-51. These primers were used in the detection of NANBH. The primers are based on the 5'-terminal region and the core protein coding region. The method allows highly sensitive
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181
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            GGAACGCCAGGCGTCCCCACAACGACGACGCCACGTCGATTTGCTCGTTGGGGCTG
                                                                                                                        CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGGATCTGTTTTCCTTGTTTTCCT
                                                                                                                                                                AGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT
gcgrrcggaagagahcrccrcgrrgcragaragagagagaragaragagagaga
                                                                                                                                                                                                                     422 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTC 476
                                                                                                                                                                                                                                                                                                                                                                   Polymerase chain reaction; PCR; primer; amplify; detection; NANBHV; non-A, non-B hepatitis virus; 5'-terminal region; core protein; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer pairs specific for non-A, non-B hepatitis virus - used for high sensitivity detection of non-A non-B (NANB) hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.1%; Score 415; DB 15; Length 2540; Best Local Similarity 94.7%; Pred: No. 5.2e-117; Matches 450; Conservative 0; Mismatches 25; Indels 0
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                                                                                                                                                                                                                                                                                   AAQ63753 standard; cDNA to mRNA; 2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the core protein coding region. detection of NANBHV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NAKA/) NAKAMURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                         JP06125777-A.
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                                                                                                                                                                      Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR; polymerase chain reaction; 8s.
GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGCTG
                       gegricgegaegacaacrecrecegrigeriggeregegecerceacecregegeca
                                                                                                                                                                                                             ATCCCGGCCATGTATCAGGTCACCGCATGGCTTCGGATATGATGATGAACTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligo-nucleotide primers - derived from and used to detect and diagnose non-A , non-B hepatitis virus
                                                                                                                                                                                                                                                                                                           Fragment of NANB hepatitis virus strain HC-J4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogikubo Y, Nakamura T;
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                          AAQ15363 standard; DNA; 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                        91EP-0305270
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/*tag= a
325..1863
/*tag= b
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-370834/51.
                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus.
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17-MAR-1992
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91JP-0191376.
    26-APR-1991;
                                                                                Detection of
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                                           Nakamura T,
                                                                                                                                                                                                                                                                                                                                                   847
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                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTGTTCACCTTCTCACCTCGCCGCATCAACAGTACAGGACTGCAACTGCTCAATCT 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCTGTTCACCTTCTCGCCTGGCCGCATGAGACAGTGCAGGACTGCAACTGCTCAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCCCGGCCATTATCAGGTCACCGCATGGCTTGGGATATGATGATGATGAACTGGTC 1304
NANB hepatitis virus strain HC-J4 was isolated from a plasma sample of a chimpanzee challenged with NANB hepatitis for infectivity but which tested negative for HCV antibody by Ortho HCV Ab ELISA test.

RNA was isolated from the sample and reverse transcribed into CDNA. The 513 amino acids encoded by the CDS were determined but are not given in the specification (and hence are not included in A Geneseq.) A study of the deduced sequence suggested that the CDS encodes NANBH virus core proteins. Primers for detecting NANB hepatitis virus were designed based on the HC-J4 sequence. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTC 476
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-A non-B hepatitis; NANBH; HCV; detection; diagnosis; screening;
                                                                                                                                        Length 1863;
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                                                                                                                                                           26; Indels
                                                                                                                    Sequence 1863 BP; 333 A; 586 C; 547 G; 397 T; 0 other;
                                                                                                                                       Score 433.4; DB 12;
Pred. No. 1.4e-116;
                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR; primer; polymerase chain reaction; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                      89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ29628 standard; DNA; 2540
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(first entry)
                                                                                                                                                          Matches 449; Conservative
                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus
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16-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                        This sequence represents the 5' region of hepatitis C virus RNA. The original sample was obtained from human and chimpanzee plasma. RNA was isolated from several samples and homology compared, and the respective sequence of about 1900 - 2500 nucleotides of the 5' terminus and 1100 nucleotides of the 3' terminus determined. The 5' region (given) contains a non-coding region of at least 340 nucleotides and a region coding for the structural protein followed by a region coding for the non-structural protein followed by a region to the sequence given in the specification). When compared with the sequence of HCV disclosed in EP-388232 this sequence showed (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                         oligo-nucleotide primers with nucleotide sequences corresp.
part. of the viral RNA
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Pred. No. 4.5e-116;
0; Mismatches 27;
                                                                                                                                                                               virus
                                                                                                                                                                               non-A, non-B hepatitis
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94.3%;
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Best Local Similarity 94.3
Matches 448; Conservative
(IMMO ) IMMUNO JAPAN INC
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                                                         Okamoto
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The present sequence comprises the nucleic acid sequence of the central fectious hepatitis C virus (HCV) genotype 1b strain CC HC-14 (ATCC 209596) that is capable of expressing this virus when the carafected into cells. HC-14 was obtained from acute phase plasma of a chimpanzee experimentally infected with serum containing of a chimpanzee experimentally infected with serum containing of HC-14/91. The claimed infectious nucleic acid sequence can be used to produce chimentic genomes (see AAX24833) consisting of the open creading frames of infectious nucleic acid sequences of other cading frames of infectious nucleic acid sequences of other cading frames of infectious nucleic acid sequences in order to produce an attenuated HCV virus suitable contained acid sequences in order to produce an attenuated HCV virus suitable containe development. Infectious nucleic acid sequences can also be used to produce attenuated virus via passage in vitro or in vivo of the viruses produced by transfection of a host cell with vivo of the viruses produced by transfection of a host cell with contained to immunise mammals, especially humans, against hepatitis C used to immunise mammals, especially humans, against hepatitis C used to immunise mammals, rath nucleic acid sequences or their concoded proteases (e.g. NS3 protease) can additionally be used to concoded proteases (e.g. NS3 protease) can additionally be used to develop screening assays to identify antiviral agents for HCV.
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                                     HCV; infectious clone; infection; diagnosis; therapy; vaccine; screening; assay; antiviral; virucide; ss.
     Infectious hepatitis C virus genotype 1b strain HC-J4 genome.
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94.1%; Pred. No. 2.1e-115;
ive 0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                Purcell RH, Yanagi M;
                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                              Location/Qualifiers
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Matches 447; Conservative
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P-PSDB; AAW98022.
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The specification describes a nucleic acid comprising a chimeric virus genome, specifically bovine viral diarrhoea virus (BVDV) genome in which the (non-)structural region has been replaced by the (non-)structural region of a hepatitis C virus (HCV) genome. The nucleic acids comprising the chimeric virus and the chimeric virus are useful for identifying cell lines capable of supporting the replication of these chimeric viruses, in screening for neutralizing antibodies to HCV of different genotypes, in the production of HCV-BVDV virions, for the development of inactivated or attenuated vaccines to prevent HCV-BVDV in a mammal, 1206 361 421 Chimeric virus; bovine viral diarrhoea virus; BVDV; hepatitis C virus; HCV; vaccine; viral inhibitor; antiviral; ss. AGCIGITICACCITICICACCICGCGGCATCAAACAGIACAGGACIGCAACTGCTCAATCT 302 CIGCITICIGITICOGCIANGIAGGIGGGGAICTGIGGGGAICTGITITICCT New nucleic acid comprising a chimeric bovine viral diarrhoea virus genome in which the (non-) structural region has been replaced by hepatitis C virus (HCV) genome useful for treating or preventing HCV GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG gegincegeaagecaachecheecgingeragenegegecheacheechagenegegecha ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTC 476 Nucleotide sequence of a hepatitis C virus (HCV) clone genotype 1b. Purcell RH; (USSH) US DEPT HEALTH & HUMAN SERVICES. Disclosure; Fig 4A-F; 97pp; English. Location/Qualifiers BP. Emerson SU, AAC86939 standard; DNA; 9595 99US-0137817 02-JUN-2000; 2000WO-US15527 (first entry) 342..9374 WPI; 2001-071081/08. signs and symptoms Hepatitis C virus. P-PSDB; AAB31170 Nam J, Bukh J, WO200075352-A2 04-JUN-1999; 14-DEC-2000 02-APR-2001 1147 (362 422 1267 AAC86939; 1087 242 182 RESULT 12 Key AAC86939 g ò 요 ò 임 g à Š

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in studying the molecular properties of HCV indirectly in vitro, and in identifying inhibitors of viral enzyme activity which would be useful as antiviral agents. Formulations or compositions comprising the chimeric virions may be used to treat or prevent the signs and symptoms of HCV. The present sequence represents a HCV clone, which is used to construct chimeric nucleic acids of the invention.
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                                                                                                                   Length 9595;
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                                                                                       Sequence 9595 BP; 1934 A; 2842 C; 2698 G; 2121 T; 0 other;
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Local Similarity 94.1%; Pred. No. 2.1e-115;
les 447; Conservative 0; Mismatches 28;
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                                                                                   The present invention relates to GB virus-B. The nucleic acid molecules of the invention are useful for indirectly studying the molecular properties of hepatitis C virus (HCV). The infectious nucleic acid sequence of the GB virus-B clone and the HCV/GBV-B chimeras may be used
           New infectious nucleic acids of the GB virus-B clone, useful for indirectly studying the molecular properties of hepatitis C virus (HCV) and in developing vaccines and therapeutics for HCV
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                                                                                                                                                               Sequence 9595 BP; 1934 A; 2843 C; 2697 G; 2121 T; 0 other;
                                                                                                                                                                                                                 Indels
                                                                                                                                     in the development of vaccines and therapeutics for HCV.
                                                                                                                                                                                       Score 430.2; DB 22;
Pred. No. 2.1e-115;
0; Mismatches 28;
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                                                            Disclosure; Fig 7; 96pp; English
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                                                                                                                                                                                                                                                                             region; type C; hepatitis; virus; HCV; vaccine; serum;
                                                  ATCCCGGCCATGTATCAGGTCACGCATGGCTTGGGATATGATGAACTGGTC
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ilarity 93.9%; Pred. No. 2.3e-115;
Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region nucleic acid fragment - for type C hepatitis
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                                                                                                                                                                                                                                                                                                                                  This mucieic acid sequence comprises the genome or infectious contains the nonstructural region of infectious genotype is contains the nonstructural region of infectious genotype is the contains the nonstructural region of infectious genotype is train HC-44 (see AAX24843). The construction of such chimeric nucleic acid sequences is expected to be of importance in studying the growth and virulence properties of HCV and in the production the growth and virulence properties of HCV and in the production of HCV suitable for conferring protection against multiple of HCV. The invention also relates to the introduction of mutations or delations into infectious nucleic acid sequences of mutations or delations into infectious nucleic acid sequences can also be used to produce attenuated virus value passage in vitro or in vivo of the produce attenuated virus values comprising one or more produced by transfection of a host cell with the infectious viruses produced by transfection of a host cell with the infectious polypeptides made from the infectious nucleic acid sequence are polypeptides made from the infectious nucleic acid sequence or also be used to immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus.
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                                                                                                                                                                                                                                   New isolated hepatitis C virus nucleic acids - used to develop products for the diagnosis, prevention and treatment of HCV infections and for developing screening assays
                                                                                                                                                                                                                                                                                                                               comprises the genome of infectious
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                                                                                                                                                           Yanagi M;
                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                   Claim 8; Fig 16A-F; 126pp; English.
                                                                                                                                                             Purcell RH,
                                                                                  98US-0014416.
97US-0053062.
                                                     98WO-US14688
                                                                                                                                                              Emerson SU,
                                                                                                                                                                                             WPI; 1999-132252/11
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                                                        16-JUL-1998;
                         28-JAN-1999
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RESULT 3
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1 (bases 1 to 492)
Gu,J.; Zhao,M.; Huang,Q.; Xu,X.; Li,Y.; Peng,Y.; Song,H.; Xiao,H.; Gu,J.; Zhao,M.; Qu,J.; Qu,J.; Song,Y.; Li,N.; Qian,B.; Liu,F.; Qu,J.; Gao,X.; Cheng,Z.; Xu,Z.; Zeng,Y.; Xu,S.; Gu,W.; Tu,Y.; Jia,J.; Fu,G.; Ren,S.; Zhong,M.; Lu,G.; Yang,Y.; Gao,G.; Wang,Z.; Zhang,Q.; Chen,S.; Han,Z. and Chen,Z. Homo sapiens CDNA BM clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV758366 BM Homo sapiens cDNA clone BMFAKA03 5', mRNA sequence.
AV758366 AV758366 GI:10916214
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Contact: Zeguang Han
Sin Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
201203, P. R. China
Fax: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM35.8"
/clone_lib="BM75.8"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
/note="Vector: pTriplEx2; Site_1 3 others
                                                                                                                                    :: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
137 g 97 t 4 others
                                                                    /tissue_type="Bone marrow"
/cell type="CD34+ hematopoietic stem/progenitor cell"
/lab host="RB35.8"
/clome_lib="BM"
/note="Vector: pTriplEx2; Site_1: sfilh; Site_2: sfill
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                     Score 67.2; DB 9; Length 488;
Pred. No. 1.1e-07;
0; Mismatches 58; Indele '
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| Organiam="Homo sapiens"
| Mol_type="mRNA"
| db xref="taxon:9606"
| clone="BMFAKA03"
     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BMFAKB03"
                                                                                                                                                                                                              Query Match 13.9%;
Best Local Similarity 67.0%;
Matches 126; Conservative (
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Homo sapiens
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Tyler.B.M., Judelson,H.S., Gijzen,M., Dean,R.A. and Waugh,M.E.
USDA-IFAFS: Expression of Phytophthora sojae genes during infection
and propagation
Unpublished
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/tissue type="infected host tissue"
/cell line=P6497"
/dev_itage="48 hour post infection"
/clone lib="psHB: Infected hypocotyl soybean host. 48 hrs
post infection"
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host. 48 hrs
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                                                                                                                                               367
                                                                                                                                                                                                                                                                                                   368 TCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCTATCCCG 427
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                                                                                                                                               308 remerecentatione de la constancia de la constanta de la co
                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Pred. No. 0.39;
0; Mismatches 143; Indels 0
                                                                            4
Length 492;
                                                                       54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
DB 9;
11.5%; Score 55.6; DB 9;
65.9%; Pred. No. 0.00016;
iive 0; Mismatches 54
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/organism="Phytophthora sc/mol_type="mRNA"
/db_txref="taxon:67593"
/clone="eHB036B09"
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FORMARD: BK reverse
Seq primer: BK reverse
High quality sequence stop: 534
Location/Qualifiers
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Tel: 540-231-7318
Email: bmtyler@vt.edu
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CD040840.1 GI:30502701
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Best Local Similarity 47.4%;
Matches 129; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phytophthora sojae
Phytophthora sojae
                Query Match
Best Local Similarity 65.9
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tyler B
Tyler lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ಡ
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ORIGIN
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Triticum.
                                                                                                                                                           AL825643
AL825643 p:234 Triticum aestivum cDNA clone A09_p234_plate_14, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV638521
AV638521 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 CATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGGGCAACTCCTCCCGTTG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 CTGGGTGGCGCTCACTCCCACGCTCGCCGCCAGGAACGCCCAGCGTCCCCACAACGACAAT 269
                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 526)
Wilson, I., Beswick, R., Shepherd, S., Barker, G., Parker, J., Owen, P.,
Edwards, D., Coghill, J., Holdsworth, M., Lenton, J., Shewry, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 CCTCCTCCCGAACCCCCCCCGGGTGGATCACGTGCGAGTTCTTCGGCAGCCCCTTCTTGCC 92
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Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales;

    (bases 1 to 399)
    Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
    Nakamura, Y. and Tabata, S.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 2;
0; Mismatches 54; Indels
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Long Ashton, Bristol BS41 9AF United Kingdom.
Location/Qualifiers
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/clone="A09_p234_plate_14"
/tissue_type="drought Giressed sefoy stage="21 days old"
/dev_stage="21 days old"
/clone_lib="p:234"
a 179 c 164 g 86 t
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AV638521
AV638521.1 GI:10781841
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    299 CTGCTGCTTCTGTTCCGCT 318
                                              67
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                                                86 GTGGTGGTGGTGCTGCT
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Best Local Similarity 57.5%;
Matches 73; Conservative
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                                                                                                                                                                                                                                                                                                                  Triticum aestivum
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ORIGIN
                                                                                                               RESULT 5
AL825643/c
                                                                                                                                                                           DEFINITION
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AV638521
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147
260 TCGATGGACCAGAAGGAGCCCCGATCATGCTGACCCCCAAGACGGTGGCCAACATCAC 319
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                                                                   190 GAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGGCCAGGAACGCC 249
                                                                                                             320 CACTACGGCGGCACCATCCTCGGCTCGAACCGTGGTGGCTTCGACGTGGACAAGATTATC 379
                                                                                                                                                      250 AGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTGCTGCTTTC 309
                                                                                                                                                                                                380 AACTICCTGACGACGACGCGTCTCGCAGGIATACGIGATCGGCGCGCGGGCACCCAC 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Citek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 CGTACCTGCGGTGGCGAGCCTCCACGAAGTGGTAGAAGCCCCTGCCGCTGCTGTTGGCGG
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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/clone="zwwwaa0131904"
/clone=lib=zwwwa0.7 1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                            310 TGTTCCGCTATGTACGTGGGGATCTCTGCGG 341
                                                                                                                                                                                                                                                                                      440 cérecceccaacaagarcressasses 471
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/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
Other GSSs: OGCBJ86TM
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BZ645446
BZ645446.1 GI:28107610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301-838-5843
Fax: 301-838-0208
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Zea mays
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BZ645446/c
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ORIGIN
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VERSION
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JOURNAL
COMMENT
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/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site-1: EcoRI; Site-2:
Xho1; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dloxide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV637983 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii AV637983 AV637983
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The First Laboratory for Plant Gene Research
The First Laboratory for District Carausa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Location/Qualifiers
/mol_type="mRNA"
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/clone="texton: Collamydomonas reinhardtii 5% CO2"
/clone="texton: pBluescriptII SK-; Site 1: EcoRI; Site 2:
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DNA. Res. 7 (5), 305-307 (2000)
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
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Email: asamizu@kazusa.or.jp, re...reinhardtii"
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Generation of expressed sequence tags from low-CO2 and high-CO2
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AV637328 Alamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii cDNA clone HC071f12_r 5', mRNA sequence.
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/clone_1bb="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed_from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 153-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 451)
Asamizu, E., Mutra, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Chlamydomonas rainhardtii
Bukaryota, Viridiplantes; Chlorophyta; Chlorophyceae; Volvocales;
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/mol_type="mRNA"
/strain="C9"
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/clone="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: AhoI; The cDNA library was constructed from cells cultured in a medium with bubbling air containing 5% carbon
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Kazusa DNA Research Institute
Yana 1532-3, Kiserazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 450)

Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,

Makamura,Y. and Tabata,S.

Generation of expressed sequence tags from low-CO2 and high-CO2

adapted cells of Chlamydomonas reinhardtii

DNA Res. 7 (5), 305-307 (2000)
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Contract: Erika Asamizu
Contract: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Fana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/note="Vector: pBluescriptII SK-; Site 1: BcoRI; Site 2:
/hol; free cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
                                                                                                                                                                                                               Contact: Brika Asamizu
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Yana 1532-3, Kisarazus.or.jp, UKL:http://www.kazusa.or.jp/en/plant/.
Email: asamizu@kazusa.
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adapted cells of Chlamydomonas reinhardtii
DNA. Res. 7 (5), 305-307 (2000)
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AV634724 GI:10778044
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/clone="HC075903 x"
/clone="teaxon" thinamy dominant reinhardtii 5% CO2"
/clone="teaxon: pBluescriptII SK-; Site 1: EcoMI; Site 2: Anote="Vector: pBluescriptII SK-; Site in EcoMI; Site 2: XhoI; The cDNA library was constructed from cells cultured in a medium with bubbling air containing 5% carbon
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Kazusa DNA Research Institute
Yana 153-3.7 Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Chlamydomonas reinhardtii

Chlamydomonas reinhardtii

Chlamydomonas reinhardtii

Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

Enkaryota; Viridiplantae; Chlamydomonas.

1 (bases 1 to 453)

Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,

Nakamura,Y. and Tabata,S.
                                                 AV637643 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii cDNA clone HC075g03_r 5', mRNA sequence.
AV637643
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Chlamydomonas reinhardtii
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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8.3%; Score 40.2; DB 9; Length 451;
Best Local Similarity 51.4%; Pred. No. 2.4;
Matches 93; Conservative 0; Mismatches 88; Indels
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/mol_type="mRNA"
/strain="C9"
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/note="Vector: pBluescriptII SK-; Site_I: EcoRI; Site_2:
Xhol; The cDNA library was constructed from calls cultured
in a medium with bubbling air containing 5% carbon
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Chlamydomonas reinhardtii
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
That Laboratory for Chiba 282-0812, Japan
Yana 1532-3, Kisarazu, Chiba 282-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                               /db_xref="texon:3055"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
/knot; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
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/clone lib="Chlamydomonas reinhardtii 5% CO2"
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Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
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/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
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Search completed: December 20, 2003, 06:54:43 Job time : 1246.55 secs

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                     GenCore version 5.1.6
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US-08-483-695-30

US-08-612-973-3

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                                                                                                                                                                           December 19, 2003, 18:11:23
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-126;
Matches 483; Conservative 0; Mismatches 0;
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US-08-612-973-11
US-08-612-973-11
Sequence 11, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REPERENCE/DOCKET NUMBER: 1487-
TELECOMMUNICATION INFORMATION:
TELEFAK: (703) 816-4000
TELEFAK: (703) 816-4000
TELEFAK: (703) 816-4000
TELEFAK: (703) 816-4000
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                         LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 9, Application US/08927597

Setent No. 6245503

PAPELICANT: MARRIERS

APPLICANT: BUSBA, MARIE-BNOS

APPLICANT: BUSBA, MARIE-BNOS

TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES 111

CORRESPONDENCE ADDRESS:

STREET: 1100 NORTH GLEBE ROAD

STREET: 11100 NORTH GLEBE ROAD
                                                                                          1 ATGCCCGGTTGCTCTTCTTTCTTCTTGGCCCTGCTGTCCTGTCTGACCAIACCA
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: DEACHTIN Release #1.0, Version #1.25 (EPO)
SOFTWARE: PATENTIN DATA:
FLING DATE:
FLING DATE:
CLASSIFICATION:
                                       Length 483;
                                     100.0%; Score 483; DB 3; Length 4:
100.0%; Pred. No. 1.1e-126;
iive 0; Mismatches 0; Indels
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APPLICATION NUMBER: US 08/612,973
                                              Query Match
Best Local Similarity 100.
Matches 483; Conservative
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Length 483
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420

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120 120 180 180

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361 CAGCTGTTCACCTTCTCACCTCGCCGCATCAAACAGTACAGGACTGCAACTGCTCAATC 420
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APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARTYNOFF, GU
APPLICANT: BUYSE, MARTYNOFF, GU
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRYA APELICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 08/612,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08927597
Patent No. 6245503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Flore
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Best Local Similarity
Matches 476; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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LOCATION:
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; LOCATION:
US-08-927-597-11
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                361
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APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PORIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CARRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDEHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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Pred. No. 3.4e-124;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                               COMPUTER READABLE PORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION DATE: IL-MAR-1996
CLASSIFICATION: 435
ATTONRY AGENT INPORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 32,205
REGISTRATION NUMBER
                                                                                                                     STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA
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Matches 476; Conservative
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Sequence 14, Application US/08470426B
; Sequence 14, Application US/08470426B
; Sequence 14, Application US/08470426B
; Patent No. 58654B
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; Patent No. 58654B
; Patent No. 58654B
; Patent No. 1000 No.
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                                                             Length 1539;
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,426B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 2-153402
APPLICATION NUMBER: 12-JUN-1990
ATTONINEY/AGENT INPORMATION:
NAME: Wellacher, Robert G.
REGISTRATION NUMBER: 20,531
                                                             Score 433.4; DB 2;
pred. No. 1.3e-112;
0; Mismatches 26;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                     Query Match
Best Local Similarity 94.5%;
Matches 449; Conservative
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US-08-470-426B-17
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Okamoto, Hiroaki
APPLICANT: Okamoto, Hiroaki
APPLICANT: Nakamura, Tetebar
TITLE OF INVENTION: OLICONUCLEOTIDE PRIMERS, AND THEIR
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-B
TITLE OF INVENTION: HEPATITIS VIRUS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young,
ADDRESSEE: L.L.P.
STREET: 1850 M Street, N.W., Suite 800
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCTGTTCACCTTCTCACCTCGGCGGCATCAAACAGTACAGGACTGCAAGTGGTCAATC 420
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             AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT
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ZIP: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CLESSIFICATION NUMBER: US/08/470,426B
FILING DATE: O6-JUN-1995
CLASSIFICATION: 536
CLASSIFICATION NUMBER: UP 2-153402
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weilacher, Robert G
REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06/59-47083.1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEFAX: (202) 659-1462
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1539 base pairs
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STRANDEDNESS: single
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APPLICANT: Bukh, Jens
APPLICANT: Bukh, Jens
APPLICANT: Bukh, Jens
APPLICANT: Buccell, Robert H.
TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: 20264276
CURRENT APPLICATION NUMBER: US/09/014,416
CURRENT APPLICATION NUMBER: US/09/0127
EARLIER APPLICATION NUMBER: US/09/0127
EARLIER APPLICATION DATE: 1997-07-18
                                                                                                                                                                                                                                                                                                                   1027 GTGTTCAGGAGGGTAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCACGCTCGCGGGCA
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                                            Length
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Pred. No. 1.8e-111;
0; Mismatches 28;
                                      Score 430.2; DB 3;
Pred. No. 1.8e-111;
0; Mismatches 28;
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Patent No. 6153421
GENERAL INFORMATION:
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Best Local Similarity 94.1%;
Matches 447; Conservative
                                      Query Match
Best Local Similarity 94.1%;
Matches 447; Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
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Patent No. 6153421

GENERAL INFORMATION:
APPLICANT: Vanagi, Masayuki
APPLICANT: Bukh, Jens
APPLICANT: Purcell, Robert H.

TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 20264276
CURRENT APPLICATION NUMBER: US 60/053,062
CURRENT APPLICATION NUMBER: US 60/053,062
EARLIER PILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 65
SEQ ID NO 4

LENGTH: 9595
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 1863;
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                                                                                                                                                                                                                                                                                                                                                                                                Score 433.4; DB 2;
Pred. No. 1.4e-112;
0; Mismatches 26;
            06/59-47083.1
REFERENCE/DOCKET NUMBER: 06/F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2811
TELEFAX: (202) 659-2811
TELEFAX: (202) 659-1462
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1863 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.5%;
Matches 449; Conservative
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CORGANISM: Hepatitis C virus
US-09-014-416-4
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US-09-014-416-4
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Score 425.4; DB 4;
Pred. No. 3.9e-110;
0; Mismatches 31;
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SEQUENCE DESCRIPTION: SEQ ID NO: 96
US-08-150-204E-96
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                                                                                              Query Match 88.1%;
Best Local Similarity 93.5%;
Matches 444; Conservative (
 TOPOLOGY: linear
MOLECULE TYPE: DNA
FRATURE:
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               GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG
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GCGTTCGGGAGGGCAACTCCTCCTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
                                                                                                                                                                                                                                                                                     ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Daejeon
STATE: Daejeon
COUNTEX: Republic of Korea
ZIP: 305-340
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: YANG, Jae Young
STREET: 386-1, Doryong-dong, Yuseong-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER: IBM PC/pentium
COMPOTER: IBM PC/pentium
OPERATIOR SYSTEM: Windows
SOFFWARE: Microsoft Word
CURRENT APPLICATION DUMBER: US/08/150,204E
PILING DATE: 20-Apr-1994
CLASSIFICATION: cUnknown>
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APPLICATION NUMBER: KR 91-9510
FILING DATE: 10-UNU-1991
APPLICATION NUMBER: KR 91-13601
FILING DATE: 6-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Shahan Islam, ESG.
REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER: 269
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TELEFAN: (212) 940-8564
INFORMATION FOR SEQ ID NO: 96
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  Sequence 96, Application US/08150204E Sequence 96, Application US/08150204E Patent No. 6538126 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CHO, Joong Myung
APPLICANT: CHO, Joong Beom
PARK, Young Woo
LIM, Kook Jin
CHOI, Deog Young
SO, Hong Seob
KIM, Chun Hyung
KIM, Sung Taek
YANG, Jae Young
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Sequence 30, Application US/08483695
Sequence 30, Application US/08483695
Sequence 30, Application
Senticant: Brechot, Christian
APPLICANT: Brechot, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Noncleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OP SEQUENCES: 46
NUMBER OP SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1267
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Length 9472;
                                           Indels
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COUNTRY: USA
COUNTRY: USA
ZIP: 20005-3315
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,695
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ATCCCGGCCATTATCAGGTCACCGCATGGCTTGGGATATGATGA 501
                                                                                                                                                                                                                                                                                                                                          NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REPERENCE, POCKET NUMBER: 05286-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Other CDNA to genomic RNA
                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 30:
                                                                                                           ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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     CORRESPONDENCE ADDRESS:
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Best Local Similarity
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DESCRIPTION:
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                                                                                                 COUNTRY:
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Hepatitis C Virus Isolate, Diagnostic and Therapeutic
Applications
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Pred. No. 2.3e-110;
0; Mismatches 25; Indels
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REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05286-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-400
TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
FILING DATE: 18-MAR-1993
APPLICATION NUMBER: PR 91 06 882
FILING DATE: 06-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30, Application US/07965285; Patent No. 5879904; GENERAL INFORMATION:
APPLICANT: Brechot, Christian APPLICANT: Kremsdorf, Dina APPLICANT: Porchon, Colette; TITLE OF INVENTION: Nucleotide and TITLE OF INVENTION: Hepatitis C Vii; TITLE OF INVENTION: Applications NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                            Other CDNA to genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.6%;
Matches 440; Conservative
                                                                                                                                                                                                                                                          LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
DESCRIPTION:
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US-07-965-285-30
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182 GCGTTCGGGAGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA 241
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ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
FILING DATE: 18-MAR-1993
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: FR 91 06 882
FILING DATE: 06-JUN-1991
ATTORNEY/AGENT INFORMATION:
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Sequence 30, Application US/09201912
Sequence 30, Application US/09201912
Sequence 30, Application US/09201912
Sequence 30, Application
Repair No. 6210962
GENERAL INFORMATION:
APPLICANT: Brechot, Chistian
APPLICANT: Remember, Dina
APPLICANT: Forchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Punnegan, Henderson, Farabow, Garrett &
ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 AGCTGTTCACCTTCTCCCCTCGCCGGCATGAGACAGTGCAGGACTGCAGGACTGCTAGATTCT 456
                                                                                                                                                                                                                                                     AGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT 421
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242 GGAACGCCAGACACACACACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG
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Best Local Similarity 94.6%; Pred. No. 2.3e-110;
Matches 440; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGA 466
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PateintIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLICASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING STENIEVENAMION:
NAME: MEYERS, Kenneth J.
NAME: MEYERS, Kenneth J.
TERISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05286-0001-00000
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION INFO
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INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
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US-09-201-912-30
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                                                                                                                   Sequence 30, Application US/08487231

Sequence 30, Application US/08487231

Patent No. 5919454

GENERAL INFORMATION:
APPLICANT: Brechot, Christian
APPLICANT: Exemadorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Notlebetide and Peptide Sequences of a
TITLE OF INVENTION: Applications
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCES: 46
CORRESPONDENCES: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 GCGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCA 276
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SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,231
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/965,285
FILING DATE: 18-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: FR 91 06 882
FILING DATE: 06-JUN-1991
ATTONEY/AGENT INFORMATION:
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Pred. No. 2.3e-110;
0; Mismatches 25;
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REGISTRATION NUMBER: 05286-0001-02000
REPERENCE/DOCKET NUMBER: 05286-0001-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 94.6%;
Matches 440; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: DC
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                                                                              RESULT 12
US-08-487-231-30
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301 GCTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCC 360
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APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GV
APPLICANT: DE WARTYNOFF, GV
APPLICANT: BUYSE, MARTYNOFF, GV
APPLICANT: BUYSE, MARTYNOFF, GV
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NRTH GLEBE ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 642;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 424.8; DB 3;
Pred. No. 2.8e-110;
0; Mismatches 32;
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Patent No. 6245503
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 93.3%;
Matches 444; Conservative
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COMPUTER READABLE FORM:
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STATE: VIRGINIA
COUNTRY: U.S.A.
    HYPOTHETICAL:
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-612-973-3
                                                                                                                   NAME/KEY:
LOCATION:
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TGCCCGGTTGCTCTTTCTCTTTCCTCTTGGCTTTGCTGTCTGTTTTGACCATCCCAG 96
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APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARTYNOFF, GUY
APPLICANT: BUYSE, MARTYNOFF, GUY
APPLICANT: BUYSE, MARTSE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUTYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION UNMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 816-4100
TELEPAX: (703) 816-4100
TELEPAX: (703) 816-4100
TELEPAX: 10400
TELE
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Patent No. 6150134
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US-08-612-973±3
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FILING DATE:

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AGGAACGCCAGCGTCCCCGACAACGACAATACGACGCCACGTCGATTTGCTCGTTTGGGGGCT 300
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                                                                                                                                                                                                                                                                               Query Match 88.0%; Score 424.8; DB 3; Length 642; Best Local Similarity 93.3%; Pred. No. 2.8e-110; Matches 444; Conservative 0; Mismatches 32; Indels 0;
PILING DATE:
CLASSIFICATION:
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
TIMBO BATE:
TIMBORE:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPRAY: (703) 816-4000
TELEPRAY: (703) 816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
TYPE: NUCLEIC acid
STRANDEDNESS: single
TYPE: NUCLEIC CONDA
HYPOTHETICAL: NO
NUTT-SENSE: NO
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FEATURE:
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, LOCATION:
US-08-927-597-3
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Search completed: December 20, 2003, 07:03:00 Job time : 35.8338 secs

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December 19, 2003, 16:55:48; Search time 1817.41 Seconds (without alignments) 10804.703 Million cell updates/sec
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1 AIGTCCGGTTGCTCTTTCTC.....TGATGATGAACTGGTAATAG 480
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                              2888711 seqs, 20454813386 residues
                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                Searched:
                                                                              Run on:
                                                                                                                                    Title:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| uo | 73 | ARIS/328 Sequence | | A48671 Sequence 9 | Sequenc | AX452/58 Sequence AX685010 Sequence | AF207766 Hepatitis | Hepatitis DNA encodi | DNA to 5' | DNA enco | Sequence | Sequence | 7 Hepatiti | 8 Hepatiti 5 Hepatiti | AF054254 Hepatitis | 2 Hepatiti Henafitis | Sequence | AF054247 Hepatitis AF054249 Hepatitis | Sequence | DNA encodi | nepacitis 1 Hepatiti | 2 Hepatiti | Hepatit 8 Hepat | equence 7 | | | 6 Hepatiti | 3 Hepatiti | 9 Hepatiti | 9 | 9 Hepatiti | 1 Hepatiti | | | 1inear DAT 07-MAR-1997 | | | | | Buyse,M. PROTEINS FOR DIAGNOSTIC AND | |
|-----------------------|--------|-------------------|------|-------------------|---------|--|--------------------|-------------------------|-----------|--------------|----------|--------------------|------------|--------------------------|--------------------|-------------------------|----------|--|----------|------------|-------------------------|------------|--------------------|-----------|------------|--------|------------|------------|------------|---------|------------|------------|------------|--------|------------------------|-------------------|---------|--------------------|-------|---|----------------------------|
| DB ID | A48673 | AR15732 | | | | | | 4 HPCSTRJ R04260 | | _ 4 | , ~ | AR027783 | 4 AF05425 | 4 AF05425 4 AF05425 | 14 AF054254 | 4 AF16505 4 HPC1491 | AR119832 | 4 4 | AR119833 | E04085 | * 4 | 4 AF05425 | 4 4 | A48669 | 6 AR157326 | AX6850 | 4 AF20775 | AB04909 | AF05425 | | AF48326 | AF16505 | ALIGNMENTS | | _ | Patent W09604385. | 2386 | | ã | V., De, M.G. and | 11 15-FEB-1996; |
| Query Match Length | 0.0 | 0.0 | 0.0 | 8.8 48 | 8.8 48 | 8.8 | 0.8 937 | 0.2 188 | 0.2 254 | 0.2 254 | 9.8 153 | 9.8 186 9.8 958 | 9.5 878 | 9.5 878 | 89.2 8781 | 9.2 937 | 9.2 959 | 9.2 959 | 9.2 959 | 8.8 57 | 8.8 877 | 8.8 878 | 8.8 941 8.8 959 | 8.8 63 | 8.8 63 | 8.8 | 8.8 937 | 8.8 943 | 8.5 878 | 8.5 878 | 8.5 936 | 8.5 937 | | | , | ce 11 from | GI:230 | 44.4 | fied. | ABES I CO 4 SDB,G., BOS FED HEPATIT | PEUTIC USE t: WO 960438 |
| Ou Score Ma | 80 1 | o c | 80 1 | 74.2 | 2.5 | 74.2 | 436 | 32.8 | 32.8 | 32.8 32.8 | 31.2 | 31.2 | | 29.6 428 | 428 | æ æ | 8 9 | 8 8 0 8 | 428 | 26.4 | 26.4 | 26.4 | 26.4 | 26.2 | ų, c | 26.2 | 426 | 426 | 24.8 | | 24.8 | 24.8 | | | 748677 | Seque | | unide | uncle | Maert PIRIE | • |
| Result No. | | 73 67 | v 4 | · ഹ | 91 | ~ 00 | , O | 10 | 12 | 13 | 15 | 16 | 18 | 19 | 21 | 22 | 24 | 25 | 27 | 28 | 30 | 31 | 33 | 34 | 35 | 37 | 38 | € 4 Ø C | 41 | 42 | 44 A | 4.4 | | RESULT | A48673 | DEFINITION | VERSION | KEYWORDS SOURCE | | AUTHORS | JOURNAL |

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Sequence 11 from Patent EP1211315.
AX452760 AX452760.1 GI:21712445
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Location/Qualifiers
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                                                                 Query Match
Best Local 9
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
                                  BASE COUNT
ORIGIN
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Matches
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
therapeutic use 6245503-A 11 12-JUN-2001;
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                                                                                                                                                                                                                                                         0; Mismatches
                    Other publication CA 2172273 960215
Other publication AU 3382495 960304
Location/Qualifiers
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                                                                                                                                                                                                                                  100.0%; Score 480;
100.0%; Pred. No. 50
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149 c 123 g
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            INNOGENETICS NV (BE)
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Best Local Similarity 100.
Matches 480; Conservative
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1. -4.74
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100.0%; Score 480; DB 6.
larity 100.0%; Pred. No. 5e-113
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Patent: WO 9604385-A 9 15-FEB-1996;
INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.
Location/Qualifiers
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Patent: WO 02055548-A 11 18-JUL-2002;
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| 121 AACTCAAGCATAGTGTATGAGGCAGCATACATCATCACACCCCGGGTGCGTGC | 121 TATCCCGGCCATGTATCAGGTCACGCATGGCTTGGGATATGATGATGATGACGGATATGATGATGATGATGATGATGATGATGATGATGATG | NISM Hepati Viruse NCE 1 ORS Maerte E Recomb NAL Patent Innoge iource | | Query Match 98.8%; Score 474.2; DB 6; Length 483; Best Local Similarity 99.4%; Pred. No. 1.6e-111; 3; Indels 0; Gaps 0; Matches 476; Conservative 0; Mismatches 3; Indels 0; Gaps 0; 0; QY 1 ATGCCGGTTGCTCTTTCTCTTTCTCTTTGGCCTGCTGTTCTGACTATCGA 60 Db 1 ATGCCGGTTGTTTTCTTTTCTTTCTTTCTTTTCTTTTGGCCTGTTTTGACATACGA 60 QY 61 GCTTCGCTTATGAAGTGGCAACGTGTCCGGGGTGTACCATGACAACGACTGCTC 120 Db 61 GCTTCGGCTTATGAAGTGGCAACGTGTCCGGGGTGTACCATGACAACGACTGCTC 120 Db 61 GCTTCCGCTTATGAAGTGGCAACGTGTCGGGGGTGTACCATGACACACGCTCC 120 C 121 AACTCAAGCATAGAGGCAACGTGTCGGGGGTGTACCATGCCCGGGTGCTCC 120 |
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Characteristics of hepatitis C viral genome associated with disease
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Nagayama, K., Kurosaki, M., Enomoto, N., Miyasaka, Y., Marumo, F. and
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                                                                                                                                                                                                                                                                                                                                                                                                                         9379 bp
Hepatitis C virus strain MD25 co
AF207766
AF207766.1 GI:7650249
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/strain="MD25"
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/codon_start=1
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/codon start=1
/protein.id="CAD86522.1"
/brotein.id="CAD86522.1"
/db_xref="G1:29374649"
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Purified Hepatitis C Virus envelope proteins for diagnostic and
                                                     AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT
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Pred. No. 1.6e-111;
0; Mismatches 3;
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/db_xref="taxon:11103"
1. 780
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Patent: WO 02055548-A 9 18-JUL-2002;
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DPPQPEYDLELITSCSSNVSVAHDASGKRYYYLTRDFTTPLARAAWETAKSTPVNSWL
GRINTWAPETHGARMILWHFFSILLAGEQLEKALDCOIYGACYSIEPLDLPQIIQRLH
GLSAFSLHSYSPCEINRVASCLRKLGYPPLRVWRLRARSVRAKLLSQGGRAATCGKYL
FNWAVKTKLKLTPIPPASQLDLSNWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGV
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AQGLIRVCMLVRKVAGGHYVQMALMKLAALTGTYVVDHLTPLRDWAHAGLRDLAVAVE
PVIFSDMETKVITWGADTAACVNIISGLPVSARRGKEILLGPADSHEGRGWRLLAPIT
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Pred. No. 1.1e-101;
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Miyakawa,Y. and Mayumi,M.
Nucleotide sequence of the genomic RNA of hepatitis C virus
isolated from a human carrier: comparison with reported isolates
for conserved and divergent regions
J. Gen. Virol. 72 (Pt 11), 2697-2704 (1991)
                                                                                                                                          HPCSTRJ4 10-MAY-1998 HNA linear VRL 16-MAY-1998 Hepatitis C virus gene for structural protein, partial cds,
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Hepacivirus
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Mink,M.A., Benichou,S., Madaule,P., Tiollais,P., Prince,A.M. and
Inchauspe,G.
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422 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGAATATGATGATGAACTGGTAA 477
1255 ATCCCGGCCACTTATCAGGTCACCGCATGGCTTGGGAATATGATGATGATGATGGTCA 1310
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Xawachi-gun, Tochigi-ken 329-04
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/mol type="genomic RNA"
/isolate="HC-J4"
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/note="82 bp upstream of
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/protein_id="BAA00706.1"
/db_xref="GI:221514"
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0285-44-1557.
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Hepatitis C virus
                                                                                                                                                                                              isolate: HC-J4.
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*source: strain=HC-J4;
Location/Qualifiers
                                           1. .2540
/note='a pi
virus'.
Location/Qualifiers
                                                                                                                                                                            90.2%;
ilarity 94.3%;
Conservative
                                            misc_feature
                                                                                                                                                                                        Similarity
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      GVNYATGNLPGCSFSIFLLALLSCLTIPASAYEVRNVSGIYHVTNDCSNSSIVYEAAD
MHTPECCPCVREDNSSEXWALLTFTLARRANSVPTTTIRKHVDLLVGAAFCSAMY
VGDLCGSVFLVSQLFFSPRRHETVQDCNCSIYPGHLSGHRMANDMANANSPTTALVV
SQLLRIPQAVUDMYAGAHWGVLAGLAYYSMVGNWARVLIVALLFAGWDGFTYTSGGAA
SGLTRIPQAVUDMYAGAHWGVLAGLAYYSMVGNWARVLIVALLFAGWDGFTYTSGGAA
GCPERMASCRPIDWFAQGWGPITYTEPDSFDQRFYCWHYAFRDSLFALFYTHRENSS
GCPERMASCRPIDWFAQGWGPITYTEPDSFDQRFYCWHYAFRDFGGIVFASGWCGFVYC
PTPSFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIGHLY SENSITIVE DETECTION METHOD OF NON-A NON-B TYPE HEPATITIS VIRUS USING OLICONUCRECTIDE PRIMER AND OLICONUCLECTIDE PRIMER
                                                                                                                                                                                                  847 receesariecterricitaterrecterrisectrisectereterrisacearceas
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                                                                                                                                                      Gaps
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                                                                                                                            Score 432.8; DB 14; Length 1880;
Pred. No. 7.4e-101;
0; Mismatches 27; Indels 0;
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NAKAWURA TETSUO
PN JP 1993023200-A/2
PD 02-FEB-1993
PF 26-APR-1991 JP 1991191376
PR 12-JUN-1990 JP 90P 153402
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Okamoto, H. and Nakamura, T.
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hypothetical: No;
anti-sense: No;
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Best Local Similarity 94.3%;
Matches 449; Conservative
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E04260
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CDNA to 5'-terminal region of gRNA of Hepatitis nonA nonB virus.

E04805.
E04805.
I GI:2173001
JP 1993091884-A/2.
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Okamoto, H. and Nakamura, T.
Okamoto, H. and Nakamura, T.
Obercitoo System FOR NON-A NON-B HEPATITIS VIRUS RELATING ANTIGEN AND AND ANTIBODY, POLYNUCLECTIDE AND POLYPEPTIDE
PATENT: JP 1993091884-A 2 16-APR-1993;
NAKAMURA TETSUO
OS HEPATILIS NONA NONB VÍTUS
PN JP 1993091884-A/2
PD 16-APR-1993
PP 10-APR-1993
PF 10-APR-1999
PF 12-JUN-1990 JP 90P 153401, 08-NOV-1990 JP 90P 304405 PI
OKAMOTO HIROAKI, NAKAMURA TETSUO
hepatitis
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non-A non-B
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  type
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Pred. No. 7.4e-101;
0; Mismatches 27;
oŧ
                                                     / . . 2540
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
a 776 c 741 g 553
  part
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VRL 01-FEB-2000
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                     F 20-UUN-1991 JP 1991247120
I OKAMOTO HIROAKI, NAKAMURA TETSUO
C C12M15/51,C12N1/21,C12P21/02,C12Q1/70,G01N33/53,G01N33/569,
G01N33/576;
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/organism='Hepatitis non-A non-B virus'
/strain='HG-J4'
1. .341
ide 342. .1040
/note='non-Structural protein of chimpar
hepatitis non-A
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Pred. No. 7.4e-101;
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/note='Structural protein
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/organism="unidentified"
/mol type="genomic RNA"
/db_xxef="taxon:32644"
a 776 c 741 g 553
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non-B virus'
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Hepatitis non-A non-B virus
JP 1994125777-A/4
10-MAY-1994
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                                                                   strandedness: Single;
                                                                           topology: Linear; hypothetical: No; anti-sense: No;
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Best Local Similarity 94.3%;
Matches 449; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unclassified.
unclassified.
1 (bases 1 to 2540)
Okamoto, H. and Nakamura, T.
OLIGONUCLEOTIDE PRIMER AND METHOD FOR DETECTING NON-A AND NON-B
TYPE HEAPITITS VIRUS IN HICH SENSITIVITY
Patent: 19 1994125777-A 4 10-MAY-1994;
NAKAMURA TEISUO
     C12N15/51,C07K13/00,C12N15/06,C12P21/08,G01N33/53,G01N33/576,
G01N33/577;
strandedness: Single;
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                                                                                                                                                                                                                                        Gaps
                                                                                TR 1. .341
342 .2540
/note='protein coded by Hepatitis nonA :
virus gene'.
Location/Qualifiers
                                                                                                                                                                                                                      .;
                                                                                                                                                                                                  Query Match

90.2%; Score 432.8; DB 6; Length 2540;
Best Local Similarity 94.3%; Pred. No. 7.4e-101;
Matches 449; Conservative 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2540 bp RNA linear P cDNA encoding chimpanzee hepatitis non-A non-B virus. B07391. B07391. GI:2175530 JP 1994125777-A/4. unidentified unclassified
                                                                 Location/Qualifiers
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/organism="unidentified"

/mol_type="genomic RNA"

/db_xref="taxon:32644"

a 776 c 741 g 553
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                                     topology: Linear;
hypothetical: No;
anti-sense: No;
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TLAGPKGPITQNYTNVDLDLVGWQAPPGARSWTPCTCGSSDLYLVTRHADVIPVRRRG
DSRGSLLSPPVSYLKGSSGGPLLCPSGHVVGVFRAAVCTRGVAKAUDFIPVESMETT
MRSPVPTDNSSPPAVOTFQVAHLHAPTGSGKSTKVPAAYAAQSYKVLVLNPSVAATL
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DHLEFWESVFTGLSHIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKC
                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Okamoto, H., Kojima, M., Okada, S., Yoshizawa, H., Iizuka, H.,
Tanaka, T., Muchmore, B.E., Peterson, D.A., Ito, Y. and Mishiro, S.
Genetic drift of hepatitis C virus during an 8.2-year infection in a chimpanzee: variability and stability
9219112
                                                                                                                                       C protein, B protein, E2 protein, NS1 protein, NS2 protein, NS9 protein, NS9 protein, NS9 protein. Heparitis C virus Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (17-OCT-1991) Hiroaki Okamoto, Jichi Medical School, Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi 329-04, Japan (E-mail:hokamotogojichi.ac.jp, Tel:0285-44-2111(ex.334), Fax:0265-44-1557) Submitted (17-Oct-1991) to DDBJ by:
Hepatitis C virus genome, complete sequence.
D13558 D01217
D13558.1 GI:221604
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protein id="BAA02756.1"
db xref="G1:221605"
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/strain="HC-J4"
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Tochigi 329-04
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YWTGALITPCAAEESALP PIPELSSTLERHHWYVATTSRSASLRQKKYTPBRLQVLD
DHYRDVLKEWKALASTWKAKLLS IEBACKLTPPBHSAKSKFGYGAKDYBNLSSBAVNH
RSVWEDLLEDTETPIDTTIMAKNEVFCVQPEKGGRKPARLI VPPDLGVR VCEKMALYD
VVSTLPQAMMGSSYGFQYSPKQRVEFLWWTWKSKKCPMGFSYDTRCPDSTVTESDIRV
EESI YQCCDLAPEARQAIRSTFRENTENTIGFPLTNSKGQNCGYRRCRAGSVTTSCGNTL
TCYLKATRACRAAKLDCTMLVNGDDLVVICESAGTQEBDAAALRVFTBAMTRYSAPPG 1026 PALASLMAFTASITSPLTTQNTLLFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSI GLGKVLVDILAGYGAGVAGALVAFKVMSGEVPSTEDLVNLLPAILSPGALVVGVVCAA ILRRHVGPGEGAVQWMNRLIAFASRGNHVSPTHYVPESDAAARVTQILSSLTITQLLK RLHQWINEDCSTPČSGSWLRDVWDWICTVLTDFKTWLQSKLLPFL.PGVPFLSCQRGYK WYRGDGINGTTCPCGAQIAGHYKNGSBNRIVOPRTCSNTWHGTPFINATTGPCTPSP APNYSBALMRVAAEFEVEVTRYGOFHYVTGWTTDNVKCPCQVBAPEFFTBVDGRLHR VAPACKPLLREDVAEFQVGLNQYLVGSQLPCEPBPDVTVLTSMLTDPSHITAETAKREL ARGSPPSLASSSASQLSAPSLKATCTTHHDSPDADLIBANLLWRQBMGGNITRVBSBN KVVILDSFBPLHABGDBRBISVAABILRKSRKFPSALPIWARPDYNPPLLESWKDPDY VPPVVHGCPLPPTKAPPIPPRRKRTVVLTBSNVSSALABLATKTFSSSGSSAVDSGT DPPQPEYDLELITSCSSNVSVAHDASGKRVYYLTRDPTIPLARAAWETARHTPVNSWL GNIIWYAPALWARMILMTHFFSILLAQEQLEQALDCQIYGACYSIEPLDLPQIIERLH GLSAFSLHSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAATCGRYL FNWAVRTKLKLTPIPAASQLDLSGWFVAGYSGGDIYHSLSRARPRWFLLCLLLLSVGV ö 1027 GCGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCACGCTCGCGGGCCA 1086 1087 GGAATGCCAGCGTCCCCACTACGACAATACGACGCCACGTCGACTTGCTCGTTGGGGCGG 1146 1147 CTGCTTTCTGCTCCGCTATGTACGTGGGGGATCTCTGCGGGATCTGTTTTCCTCGTCTCCC 1206 996 121 181 61 847 IGCCCGGTTGCTCTTCTTTCTTCTTTGGCTTTGCTGTCCTGTTTGACCATCCCAG 62 CTTCCGCTJATGAAGTGCGCAACGTGTCCGGGGTGTACATGTCACGACGACTGCTCCA 2 TGTCCGGTTGCTCTTTCTTTCTTTCGCCCTGCTGTCCTGTCTGACCATACCAG 182 GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA 242 GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTCCTTGTTTCCC /note="possible stem-loop structure in NS4 sequence" 9413. 9448 /note="T-stretch of 36 bp". a 2828 c 2676 g 2045 t 90.2%; Score 432.8; DB 14; Length 9448; 94.3%; Pred. No. 7.6e-101; o; Mismatches 27; Indels 0; 342. .914 /product="C protein" 915. .1490 /product="E protein" 1491. .2528 /product="NS1/E2 protein" /product="NS2 protein" 3360. .5186 5187. .6380 /product="NS4 protein" 6381. .9371 /product="NS5 protein" 1360. .5186 'product="NS3 protein" .3359 6005. .6104 GIYLLPNR" 449; Conservative Local Similarity 1899 a misc_feature mat_peptide mat_peptide mat_peptide mat_peptide mat_peptide mat_peptide mat_peptide stem_loop 302 Query Match BASE COUNT ORIGIN Best Loca Matches

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CIGCITICIGITCCGCIAIGIACGIGGGGAATCICIGCGGAICTGITTICCITGITICC 361
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                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                     Unclassified.

1 (bases 1 to 1539)
Okamoto, H. and Nakamura, T.
Oklogonucleotide primers, and their application for high-fidelity
Oligonucleotide primers, and their application for partitity
detection of non-A, non-B hepatitis virus
Patent: US 5856458-A 17 05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       422 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTAA 477
1267 ATCCCGGCCATTTATCAGGTCACCGCATGGCTTGGGATATGATGATGATGATGATCACTCGTCA 1322
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Best Local Similarity 94.1%; Pred. No. 1.9e-100;
Matches 448; Conservative 0; Mismatches 28; Indels
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Sequence 17 from patent US 5856458.
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Scoring table:

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HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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                                                                                                                                                                                                                                       1 ATGTCCGGTTGCTCTTTCTC.....TGATGATGAACTGGTAATAG 480
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                 GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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474.2 432.8 432.8 432.8

Score

Result SO.

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AATI2704-T12709 and AATI2961-T12974 represent hepatitis C virus (HCV) E1 and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E31, E2, and E41/E2 proteins. C in vectoris for the production of recombinant E31, E2, and E41/E2 proteins. C invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage agent, after 1981s of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated constructs of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated by known are meantly and and an erra than those isolated by known
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proteins - in presence of dissulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 480 BP; 85 A; 149 C; 123 G; 123 T; 0 other;
                                                                                            Claim 23; Fig 21; 146pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for invitro monitoring of HCV disease or prognosing the response to in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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 Hepatitis C virus, HCV, B1 protein; B2 protein; infection; gene; virucide; immunostimulant; vaccine; ds.
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30-AUG-2001; 2001US-315768P.
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Best Local Similarity
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                                                   Hepatitis C virus
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480
                                                                                                                                                              480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; humar serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                                                                                                       421 TATCCCGGCCATGTATCAGGTCACCGCATGGCTTAGGATATGATGATGATGATGGTAATAG
                                                                                               TATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purifying recombinant hepatitis C virus (HCV) B1 and B2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 483 BP; 85 A; 152 C; 123 G; 123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maertens G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Martynoff G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 23; Fig 21; 146pp; English.
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                                                                                                                                                                                                                                                                                                           AAT12707 standard; DNA; 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buyse M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-129401/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             assays of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-1995;
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are
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                                                                                                                                                                                                                                                                                                                                                                                                                        421 TATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGATGACTGGTCCTA 479
                                                                                                                                                                                                             TGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCC
                                                                                                                                           TGCGTTCGGGAGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCCACGCTCGCGGCC
                                                                                                                                                                                       241 AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT
                                                                                                                                                                                                                                                         GCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGGATCTGTTTTCCTTGTTTCC
                                                                                                                                                                                                                                                                          361 CAGCTGTTCACCTTCTCACCTCGCCGCATCAAACAGTACAGGACTGCAACTGCTCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; E1 protein; E2 protein; infection; gene; virucide; immunostimulant; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus clone HCCI12A El protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 165-166; 243pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bosman F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-599657/64.
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Gaps

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Indels

Length 483;

DB 17;

Score 474.2; DB 17 Pred. No. 9.4e-129; 0; Mismatches 3;

Query Match
Best Local Similarity 99.4%;
Matches 476; Conservative

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1 AIGICCGGTIGCICITICICIAICTICCICITIGGCCCIGCIGICCIG

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AGGAACGCCAGGGTCCCCACAACGACAATACGACGCCCACGTCGATTTGCTCGTTGGGGCT 300
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useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                                                                                                                           TCTCTATCTTCCTTTGGCCCTGCTGTCTGACCATACCA
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                                                                                                   Score 474.2; DB 24; Length 483; Pred. No. 9.4e-129; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amplification
                                                                                  Sequence 483 BP; 85 A; 152 C; 123 G; 123 T; 0 other;
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polymerase chain reaction; vaccine; antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatitis virus strain HC-J4 genome
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/label= HC-J4
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                                                                                                       Query Match
Best Local Similarity 99.4%;
Matches 476; Conservative
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                                                                                                                                                  1 ATGTCCGGTTGCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                     This sequence is the genome of the non-A, non-B hepatitis virus (NANBHV) strain HC-J4. This sequence was derived by amplification by polymerase chain reaction. The nucleotide sequences derived from this amplification can be used to detect NANBHV infection which could not be detected by conventional methods. The detection kits allow highly specific and sensitive detection at an early phase of infection. The polypeptide product of this coding sequence can be used for the manufacture of vaccines and immunological pharmaceuticals and also to produce antibodies specific to NANBHV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1207 AGCTGTTCACCTTCTCGCCTCGCCGCATGAGACAGTGCAGGACTGCAGCTGCTCAATCT
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                                                                                                                                                                                                                                   Recombinant cDNA of NANBH virus strain HC-J5 and corresp. peptides - useful for diagnosis and in vaccines and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1880;
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2e-116;
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Pred. No. 2e-11
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 11; 42pp; English
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                                                   (IMMO ) IMMUNO JAPAN INC
                                                                                                                Okamoto
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  08-NOV-1990;
                                                                                                                  Nakamura T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of NANB hepatitis virus polynucleotide N-2540-2 which codes for a non-A, non-B (NANB) hepatitis virus gene HC-OM. The polypeptide it encodes may be used in a system for detecting NANB hepatitis. This method is highly specific and sensitive, and can detect NANB hepatitis virus which could not be detected by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen related to non-A and non-B hepatitis virus - comprises on-translation region comprising 340 - 341 mols. of nucleotides, non-translation region comprising 1885 - 2551 mols. of nucleotides including region 1,149 and, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 432.8; DB 14; Length 2540;
Pred. No. 2.2e-116;
0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                         terminal of NANBH virus RNA'
                                                                                                                                                          Non-A, non-B; virus; polymerase chain reaction; detection; sensitive; specific; HCV; NANBH; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2540 BP; 471 A; 775 C; 741 G; 553 T; 0 other;
                                                                                                                                NANB hepatitis virus polynucleotide N-2540-2
                                           AAQ43889 standard; cDNA to mRNA; 2540 BP
                                                                                                                                                                                                                               Location/Qualifiers
342..2540
/*tag= a
1..341
/*tag= b
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                                                                                                                                                                                                                                                                                                        /note= "from 5'
                                                                                                                                                                                                      Non-A, non-B hepatitis virus
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Best Local Similarity 94.3%;
Matches 449; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              91JP-0196175,
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90JP-0304405
                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NAKA/) NAKAMURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAR38279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 432.8; DB 19; Length 2187;
Pred. No. 2.1e-116;
0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                            Cuticle protein 1 and 2 secreting hepatitis C virus (Japanese)
 dв.
protein 1; cuticle protein 2; hepatitis C virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2187 BP; 406 A; 669 C; 631 G; 481 T; 0 other;
                                                                                                              /partial
/note= "no stop codon"
                                                                                 /*tag= a
/product= "AAM47264"
                                              Location/Qualifiers
1...2187
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 2-4; 7pp; Korean.
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Best Local Similarity 94.3
Matches 449; Conservative
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P-PSDB; AAM47264.
                                                                                                                                                                                                                                                                        (GLDS ) LG CHEM LTD
                                                                                                                                                                                                                                                                                                     Choo SH, Lee IH,
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                                                                                                                                                                                                                  19-MAR-1996;
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                         Unidentified
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                                                                                        GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG 301
                                                                                                                                                                                                                                                               NANB hepatitis virus strain HC-J4 was isolated from a plasma sample of a chimpanzee challenged with NANB hepatitis for infectivity but which tested negative for HCV antibody by Ortho HCV Ab ELISA test. RNA was isolated from the sample and reverse transcribed into cDNA. The 513 amino acids encoded by the CDS were determined but are not given in the specification (and hence are not included in A-Geneseq). A study of the deduced sequence suggested that the CDS encodes NANBH virus core proteins. Primers for detecting NANB hepatitis virus were
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                                                                                                                                                                                            AGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTAATCT
                                        GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCCA
                                                                                                                                                                                                                                             ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTAA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-transfusion; non-A, non-B hepatitis; HCV; detection primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detect and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligo-nucleotide primers - derived from and used to diagnose non-A , non-B hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                            Fragment of NANB hepatitis virus strain HC-J4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                      AAQ15363 standard; DNA; 1863 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymerase chain reaction; ss
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/*tag= a
325..1863
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
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17-MAR-1992
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                                                                         361
                                                                                                                           AGCTGTTCACCTTCTCACCTCCCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT 421
                        242 GGAACGCCAGCACCCCACAACGACAATACGACGCCACGTCGATTTGCTTGGGGGCTG 301
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                                                                                          ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTAA 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer pairs specific for non-A, non-B hepatitis virus - used for high sensitivity detection of non-A non-B (NANB) hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 432.8; DB 15; Length 2540;
Pred. No. 2.2e-116;
0; Mismatches 27; Indels 0;
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                                                                                                                                                                                                                                                                        AAQ63753 standard; cDNA to mRNA; 2540 BP
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ilarity 94.3%;
Conservative (
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detection of NANBHV.
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Matches 449; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NAKA/) NAKAMURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                         JP06125777-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-A non-B hepatitis; NANBH; HCV; detection; diagnosis; screening;
PCR; primer; polymerase chain reaction; ss.
                                               DB 12; Length 1863;
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                                                               Indels
                                Sequence 1863 BP; 333 A; 586 C; 547 G; 397 T; 0 other;
                                                       .8e-116;
es 28;
designed based on the HC-J4 sequence. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                              Score 431.2; I
Pred. No. 5.8e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus HC-J4 5' region.
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                                               89.8%;
94.1%;
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                                                              tches 448; Conservative
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                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus.
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16-MAR-1993
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                                                                                                                                                                                  This sequence represents the 5' region of hepatitis C virus RNA. The original sample was obtained from human and chimparazee plasma. RNA was isolated from several samples and homology compared, and the respective sequence of about 1900 - 2500 nucleotides of the 5' region (given) contains a non-cading region of at least 340 mucleotides and a region coding for the structural protein followed by a region coding for the non-structural protein (none actually detailed on the sequence given in the specification). When compared humblogy of 80.5%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 2540;
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Detection of non-A, non-B hepatitis virus - using new oligo-nucleotide primers with nucleotide sequences corresp. part. of the viral RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2540 BP; 472 A; 775 C; 741 G; 552 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 89.5%; Score 429.6; DB 13; Best Local Similarity 93.9%; Pred. No. 1.9e-115; Matches 447; Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                               Disclosure; Page 18; 54pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence comprises the nucleic acid sequence of the genome of infectious hepatitis C virus (HCV) genotype lb strain HC-J4 (ArCC 209596) that is capable of expressing this virus when transfected into cells. HC-J4 was obtained from acute phase plasma of a chimpanzee experimentally infected with serum containing of a chimpanzee experimentally infected with serum containing to produce chimeric genomes (see AAX24833) consisting of the open comproves of infectious nucleic acid sequences of other reading frames of infectious nucleic acid sequences of other comproves (including genotypes 1-6) and subtypes (such as lb, 2a, 2a, 2a, 3a, 4a-f, 5a and 6a) of HCV. The invention also relates to the introduction of mutations or deletions into infectious nucleic acid sequences can each sequence in order to produce an attenuated HCV virus suitable controlled to produce attenuated virus via passage in vitro or in also be used to produce attenuated virus via passage in vitro or the infectious nucleic acid sequence are comprising one or the infectious mucleic acid sequences con sead to induce protective controlled sequences can shalp be used to immunise mammals, especially humans, against hepatitis C cused to immunise mammals, especially humans, against hepatitis C cused to immunity against the virus. The nucleic acid sequences can also be used to induce protective immunity against the virus. The nucleic acid sequences or their concoded proteases (e.g. NS3 protease) can additionally be used to develop screening assays to identify antiviral agents for HCV.
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                                                                                                                                                                                                                                                                                                                                                       New isolated hepatitis C virus nucleic acids - used to develop products for the diagnosis, prevention and treatment of HCV infections and for developing screening assays
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Best Local Similarity 93.7%; Pred. No. 9.1e-115;
Matches 446; Conservative 0; Mismatches 30; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9595 BP; 1934 A; 2842 C; 2698 G; 2121 T; 0 other;
                                                                                                                                                                                                                                                                      Yanagi M;
                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
Location/Qualifiers
342..9374
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 14A-F; 126pp; English.
                                                                                                                                                                                                                                                                      Purcell RH,
                                                                                                                                               98WO-US14688
                                                                                                                                                                                 98US-0014416
97US-0053062
                                       /*tag=
                                                                                                                                                                                                                                                                          Emerson SU,
                                                                                                                                                                                                                                                                                                            WPI; 1999-132252/11.
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                                                                                                                                                                                   27-JAN-1998;
18-JUL-1997;
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The specification describes a nucleic acid comprising a chimeric virus genome, specifically bovine viral diarrhoea virus (BVDV) genome in which the (non-)structural region has been replaced by the (non-)structural region has been replaced by the (non-)structural region of a hepatitis C virus (HCV) genome. The nucleic acids comprising the chimeric virus and the chimeric virus and the chimeric virus and the chimeric virus supporting the replication of these chimeric viruse, in screening for neutralizing antibodies to HCV of different viruses, in screening for neutralizing antibodies to HCV of different contributed or attenuated vaccines to prevent HCV-BVDV in a mammal, of inactivated or attenuated vaccines to prevent HCV-BVDV in a mammal, of inactivated or attenuated vaccines to prevent HCV-BVDV in a mammal, of inactivated or attenuated vaccines to prevent HCV-BVDV in a mammal, and attivity in hibbitors of viral enzyme activity which would be useful as antiviral agents. Formulations or compositions comprising the chimeric virions may be used to treat or prevent the signs and symptoms of HCV. The present sequence represents a HCV clone, which is used to construct chimeric nucleic acids of the invention. 1207 AGCTGTTCACCTTCTCGCCTCGCCGCCATGAGACAGTGCCAGACTGCAACTGCTAATCT 1266 1087 GGAATGCCAGGTCCCCACTACGACAATACGACGCCACGTCGACTTGCTCGTTGGGACGG 1146 421 Chimeric virus; bovine viral diarrhoea virus; BVDV; hepatitis C virus; HCV; vaccine; viral inhibitor; antiviral; ss. 362 AGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGGTCAATCT New nucleic acid comprising a chimeric bovine viral diarrhoea virus genome in which the (non-)structural region has been replaced by hepatitis C virus (HCV) genome useful for treating or preventing HCV CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGGATCTGTTTCCTTGTTTCCC ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGGATATGATGAACTGGTAA 477 Nucleotide sequence of a hepatitis C virus (HCV) clone genotype lb. Purcell RH; (USSH) US DEPT HEALTH & HUMAN SERVICES Disclosure; Fig 4A-F; 97pp; English. Location/Qualifiers 342..9374 /*tag= a BP Emerson SU, AAC86939 standard; DNA; 9595 99US-0137817. 02-JUN-2000; 2000WO-US15527. (first entry) WPI; 2001-071081/08. P-PSDB; AAB31170. signs and symptoms Hepatitis C virus. Bukh J, WO200075352-A2 04-JUN-1999; 02-APR-2001 14-DEC-2000. 302 AAC86939; 422 Nam J, RESULT 12 AAC86939 유 ð 셤 g à à

Sequence 9595 BP; 1934 A; 2842 C; 2698 G; 2121 T; 0 other;

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of the invention are useful for indirectly studying the molecular properties of hepatitis C virus (HVV). The infectious nucleic acid sequence of the GB virus-B clone and the HCV/GBV-B chimeras may be in the development of vaccines and therapeutics for HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV; infectious clone; infection; diagnosis; therapy; vaccine;
screening; assay; antiviral; virucide; ss.
                                                                                  Length 9595;
                                                         Sequence 9595 BP; 1934 A; 2843 C; 2697 G; 2121 T; 0 other;
                                                                                                        Indels
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                                                                               Similarity 93.7%; Pred. No. 9.1e-115; 6; Conservative 0; Mismatches 30;
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97US-0053062.
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18-JUL-1997;
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Best Local Simi
Matches 446;
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                                                                     GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG
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                                                         GCGTTCGGGAGGCCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
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                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New infectious nucleic acids of the GB virus-B clone, useful for indirectly studying the molecular properties of hepatitis C virus and in developing vaccines and therapeutics for HCV
                                  ö
           Length 9595;
                                  Indels
                                    30;
         Score 428; DB 22;
Pred. No. 9.1e-115;
0; Mismatches 30;
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        89.2%;
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         Query Match
Best Local Similarity 93.7
Matches 446; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF23492 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-091214/10
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                                                                                                                                                                                                                                              This nucleic acid sequence comprises the genome of infectious hepatitis C virus (HCV) chimeric 1a/1b clone pH77C-J4 which contains the nonstructural region of infectious genotype Is strain H77 (see AAX24812) and the structural region of infectious genotype is strain HC-J4 (see AAX24843). The construction of such chimeric be strain HC-J4 (see AAX24843). The construction of such chimeric incless expended to be of importance in studying the graph of the growth and virulence properties of HCV and in the production of HCV suitable for conferring protection against multiple of HCV suitable for conferring protection against multiple of HCV suitable for conferring protections sucleic acid sequences in order to produce an attendant also relates to the introduction of morder to produce an attendant expendence and also be used to incless produced by transfection of a host cell with the infectious viruses produced by transfection of a host cell with the infectious polypeptides made from the infectious nucleic acid sequences are long or more or more polypeptides made from the infectious nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity against the virus. The nucleic acid sequences or their immunity and the virus is the virus and the virus and the virus and the virus and the virus
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                                                                                                                       New isolated hepatitis C virus nucleic acids - used to devel
products for the diagnosis, prevention and treatment of HCV
infections and for developing screening assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9599 BP; 1889 A; 2873 C; 2724 G; 2113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.7%; Pred. No. 9.1e-115;
Matches 446; Conservative 0; Mismatches 30; Indels
              Yanagi M;
                                                                                                                                                                                                                    Claim 8; Fig 16A-F; 126pp; English
              Purcell RH,
                Emerson SU,
                                                              1999-132252/11
                                                                                   P-PSDB; AAW98021
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                                                                                                                                                                                                                                                                                The sequences given in AAQ35077-89 are probes which were used to in the isolation of a novel nucleic acid encoding an envelope region of type C hepatitis virus (HCV). The isolated fragment can be used for the preparation of a vaccine for hepatitis C. The envelope region DNA for was derived from the serum of non-A, non-B hepatitis
                                                                       vaccine; serum;
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0
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                                                                                                                                                                                                                                  Envelope region nucleic acid fragment - for type C hepatitis
virus (1), for producing vaccine
                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                        31; Indels
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                                                                                                                                                                                                                                                                                                                                                                       DB 14;
                                                                                                                                                                                                                                                                                                                                                                     Score 426.4; DB 14,
Pred. No. 9.7e-115;
0; Mismatches 31;
                                                                      Envelope, region; type C; hepatitis; virus; HCV;
                                                                                                                                                                                                                                                                    Disclosure; Page 10; 13pp; Japanese.
BP
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Best Local Similarity 93.5%;
Matches 445; Conservative
577
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                                                       HCV envelope region probe
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                                     (first entry)
 AAQ35081 standard; DNA;
                                                                                                                                                                                                                      WPI; 1993-022708/03.
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                                                                                    non-A, non-B;
                                                                                                                                                               29-MAY-1991;
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                                                                                                                          JP04349885-A
                                     20-MAY-1993
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                                                                                                       Synthetic.
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                    AAQ35081;
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AV637259 AV637328

AV637983 AV637259 AV637328 AV637643 AV634724

Title:

Run

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)

Gu, J., Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H., Yi., Xu, S., Gu, W., Tu, Y., Yu, S., Gu, W., Tu, Y., Jia, J., Ru, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gao, G., Wang, Z., Zhang, Q., Chen, S., Han, Z. and Chen, Z. Homo sapiens cDNA BM clones

In Unpublished

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

201203, P. R. China

Chinese National Human Genome Center at Shanghai

201203, P. R. China

Tel: 86-21-50801992

Email: hanz@chgc:sh.cn

This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                    AV755731 AV Homo sapiens cDNA clone BMFAKB03 5', mRNA sequence.
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                                                                                                                            AV632335 ·
AV387329
BX421743
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CD206870
CB924688
AV633658
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B2578381
B2555011
CNS01213
BZ530934
AV634529
CA618797
BX415186
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AV639153
BJ209795
                                                                                                                                                                                                                                                                  AV638474
AV641448
BX391120
CNS0060N
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AV634095
AV641895
AV638125
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               Homo sapiens (human)
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EST
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VERSION
SOURCE
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JOURNAL
COMMENT
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               CD040840 psHB036xB
BZ645446 OGCBJ86TC
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AV758366 AV758366
                                                2003, 18:03:34 ; Search time 1234.83 Seconds (without alignments) 9447.586 Million cell updates/sec
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Compugen Ltd.
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      version 5
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Listing first 45 summaries
                                   sw model
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                                                                              US-09-899-303A-11
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em_gss_pln:*
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11.4
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54.6
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Result Š.

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BX391120 BX391120 AL065629 Drosophil BM868105 mgcs013xI CA487901 AGENCOURT

AV637050 AV637050
AV635382 AV635382
AV632812 AV635382
AV632811 AV632811
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AV63405 AV641895
AV641895 AV641895
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AV641895 AV641895
AV631329 AV831329
BX421743 BX421743
AL565958 AL565958
CD206870 HS1 25 D0
CB206870 HS1 25 D0
CB206870 HS1 25 D0
CB206870 AV631837
AL565958 AL565958
CB57655 OSJUBCC13C
BZ578381 BS1 BS1 BS1 BZ55011
BZ55011 Bacs1-60
AL101589 Dxcsophil
BZ55011 Dacsdy17
AV634529 AV634529
CA618797 W11n.pk00
BX418186 BF1 34 C0
AV639153 AV638474
AV638474 AV638474
AV638474 AV638474

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BASE COUNT
ORIGIN
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AUTHORS
TITLE
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COMMENT
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CD040840
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1 (bases 1 to 492)

14, 7, Zhao, M., Hung, O., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H., Gu, Y., Li, N., Olan, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gao, G., Wang, Z., Zhang, Q., Chen, S., Han, Z. and Chen, Z. Unpublished
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                                                                                                                                                                                                                                                               351
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Contract: Zeguang Han
Contract: Zeguang Han
Contract: Zeguang Han
Contract: Zeguang Han
Sist Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801920
Fax: 86-21-50801922
Email: hanzg@chgc:sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
125 g 112 t 3 others
                                                                      /tissue_type="Bone marrow"
/call type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM35.8"
/clone_lib="BM"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
134 c 137 g 97 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV758366 AW Homo sapiens CDNA clone BMFAKA03 5', mRNA sequence.
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="BRNA3"
/tissue type="Bone marrow"
/cell type="CD34+ hematopoietic stem/progenitor cell"
/lab fost=#BNS.8"
/clone llb="BM"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfill
                                                                                                                                                                                                                                                                                                                              CTTGTTTCCCAGCTGTTCACCTTCTCACCTCGCCGCATCAAACAGTACAGGACTGCAAC
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                                                                                                                                                                                                                                  4;
                                                                                                                                                                                              Score 65.8; DB 9; Length 488;
Pred. No. 2.3e-07;
0; Mismatches 57; Indels ...
      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BMFAKB03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV758366
AV758366.1 GI:10916214
                                                                                                                                                                                                      Query Match
Best Local Similarity 67.0%;
Matches 124; Conservative 0
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CTGGT 291
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Eukaryota; stramenopiles, Oomycetes; Pythiales; Pythiaceae; Phytophthora; stramenopiles; Oomycetes; Pythiaceae; Phytophthora; Stramenopiles; Oomycetes; Pythiaceae; Phytophthora; Pythiaceae; Pythiaceae; Phytophthora; Dean, R.A. and Waugh, M.E. Tyler, B.M., Judelson, H.S., Gijzen, M., Dean, R.A. and Waugh, M.E. USDA-IFAFS; Expression of Phytophthora sojae genes during infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
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1 host. 48 hrs
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/cell line="P649"
/dev Stage="48 hour post infection"
/clone_lib="psHB: Infected hypocotyl soybean host. 48 hrs
                                                                                  2
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                                                                                                                                                                     367
                                                                                                                                                                                                                                                   457 igigaricagercaeracerateresacererecerresesiareserriseaseceaaerea 398
                                                                                                                                                                                                                                                                                                                                          368 TCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCTATCCCG 427
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                                                                                                                                                                     308 ICTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCCCAGCTGT
                                                                                       Gaps
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0
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         Length 492;
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9.0%; Score 43.2; DB 14;
Best Local Similarity 47.4%; Pred. No. 0.36;
Matches 129; Conservative 0; Mismatches 143;
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Tel: 540-231-7318
Email: bmtyler@vt.edu
Score 54.6; DB 9;
Pred. No. 0.00027;
0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Phytophthora
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="8HB036B09"
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Plate: 036 row: B column: 09
Seg primer: BK reverse
High quality sequence stop: 534.
Location/Qualifiers
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CD040840.1 GI:30502701
                      11.4%;
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                           Query Match
Best Local Similarity 65.7
Matches 111; Conservative
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Tyler lab
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooideae;
Triticcae; Triticum.
Triticcae; Triticum.
I (bases 1 to 526)
Wilson, I., Beswick, R., Shepherd, S., Barker, G., Parker, J., Owen, P., Edwards, D., Coghill, J., Holdsworth, M., Lenton, J., Shewry, P. and
                                                                                                                                                              AL825643
AL825643 p:234 Triticum aestivum cDNA clone A09_p234_plate_14, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
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Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohyama, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 399)
Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.
Nakamura,Y. and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 CATGATCATGCACCCCCGGGTGCGTGCCTGCGTTCGGGAGGGCAACTCCTCCCGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 CTGGGTGGCGCTCACTCCCACGCTCGCGGCCAGGAACGCCAGCGTCCCCACACGACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A BBSRC-funded wheat BST resource for the academic community Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9; Length 526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Indels
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Long Ashton, Bristol BS41 9AF United Kingdom.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .526
/organism="Triticum aestivum"
/mol type="mRNA"
/cultivar="mercia"
/cultivar="mercia"
/clone="A09_p234_plate_14"
/tissue type="drought stressed sefuever a type="arought stressed sefuever a type="21 days old"
/clone_lib="p:234"
a 179 c 164 g 86 t
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Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                Triticum aestivum (bread wheat)
         299 CTGCTGCTTTCTGTTCCGCT 318
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AV638521.1 GI:10781841
                                                                                                                                                                                                                                                      AL825643.1 GI:21837164
                                                     86 GIGGIGGIGGIGCIGCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.5%;
Matches 73; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Barker G
                                                                                                                                                                                                                                                                                                                            Triticum aestivum
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                                                                                                                                                                                                          sequence.
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KEYWORDS
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                                                                                                                 RESULT 5
AL825643/c
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DEFINITION
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OGCBJ86TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0133P04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD calde, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 664)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Robling, D. and Lakey, N.
Consortium for Maize Genomics
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260 TCGATGGACCAGAAGAGGCCCCGATCATGCTGACCCCCCAAGACGGTGGCCAACATCAC 319
                                                                                                                                                           250 AGCGTCCCCACAACGACAATACGACGCCCACGTCGATTTGCTCGTTGGGGCTGCTGTTTC 309
                                                                     190 GAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCAGGAACGCC 249
                                                                                                               380 AACTICCIGACGACGACGCGTCTCGCAGGIATACGIGATCGGGCGGTGACGGCACCCAC 439
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/clone_lib="ZM 0.7_1.5_KB"
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methylation filtered genomic DNA library"
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Location/Qualifiers
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BZ645446.1 GI:28107610
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Contact: Cathy Whitelaw
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Fax: 301-838-0208
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/db xref="taxon:3055"
/clone="HC080c04_r"
/clone lib="Chlamydomonas reinhardtii 5% CO2"
/clone lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site 1: EcoRI; Site_2:
Xho1; The cDNA library was constructed_from cells cultured
in a medium with bubbling air containing 5% carbon
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AV637983.1 GI:10781303
BST.
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The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

Location/Qualifiers
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI;
/note="vector: pBluescriptII SK-; Site_1: acolls cultured
/note="medium with bubbling air containing 5% carbon
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Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Chlamydomonadaceae; Chlamydomonas.
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/mol_type="mRNA"
/strain="C9"
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/clone="Ht0081d07"
/clone lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site 1: EcoRI; Site 2:
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/not = "Vector: pBluescriptII SK-; Site 1: EcoRI; Site 2:
/note="vector: pBluescriptII SK-; Site 1: EcoRI; Site 2:
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Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 434)
Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamuza,Y. and Tabata,S.
Ageneration of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DAR Res. 7 (5), 305-307 (2000)
                                                             adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
20539644
10169912.
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute 292-0812, Japan
Bmail: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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    434
/organism="Chlamydomonas reinhardtii"

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VERSION
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유 ò g 8 윱 ò 셤

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/db_xref="taxon:3055"
/clone="MC01fil2 r"
/clone lib="Chlamydonnas reinhardtii 5$ CO2"
/note="Vector: pBluescriptII 5K-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5$ carbon
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The First Laboratory for Plant Gene Research
Kazuaa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Asamizu, E., Mutra, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
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Chlamydomonas reinhardtii
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Chlamydomonadaceae; Chlamydomonas.
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                150 CATGATCATGCACACCCCCGGGTGCCTGCCTTCGGGAGGGCAACTCCTCCCGTTG
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/mol_type="mRNA"
/strain="C9"
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Kazusa DNA Research Institute
Yana 1532-3, Kiearazu, Chiba 292-0812, Japan
Email: asemizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/clone="WirtoY0906 In"
/clone lib="Chamydomonas reinhardtii 5$ CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_1: a needium with bubbling air containing 5$ carbon dioxide"
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Chlamydomonadaceae; Chlamydomonas.
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Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
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/mol_type="mRNA"
/strain="C9"
                DB 9;
            ch 8.4%; Score 40.2; DE Similarity 51.4%; Pred. No. 2.2; 93; Conservative 0; Mismatches
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Best Local Similarity
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Contact: Erika Asamizu
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The First Laboratory for Plant Gene Research
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Kazusa DNA Research Institute
Yana 1532-3, Kisarzau, Chiba 292-0812, Japan
Yana 1532-3, Kisarzau, Chiba 292-0812, Japan
Location/Qualifiers
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Location/Qualifiers
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Lorganism="Chilamydomonas reinhardtii"

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Alone="Wector: pBluescript! SK-; Site_1: Ecok! Site_2:

Anote="Wector: pBluescript" SK-; Site_1: Ecok! Stie_2:

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Contact: Erika Laboratory for Plant Gene Research
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Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizukazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Nakamura, Y. and Tabata, S.
Beneration of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
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Pred. No. 2.3;
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in a medium with bubbling air containing 5% carbon
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Chlamydomonas reinhardtii
Bukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
I (bases 1 to 453)
Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
                                                                                             AV637643 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
CDNA clone HC075g03_r 5', mRNA sequence.
AV637643
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 153-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizuskazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Best Local Similarity 51.4%; Pred. No. 2.3;
Matches 93; Conservative 0; Mismatches 88; Indels (
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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1 (base 1 to 473)
Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K., Nakamura,Y. and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii

DNA Res 7 (5), 305-307 (2000)
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/note="Wector: pBluescriptII SK-; Site 3: Arbor in a medium with bubbling air containing 5% carbon dioxide"
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute Distribute DNA Research Institute 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
/hob; The cDNA library was constructed from cells cultured in a medium with bubbling air containing 5% carbon dioxide"
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Chlamydomonadacae; Chlamydomonas.
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Asamiau, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
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Search completed: December 20, 2003, 06:54:43 Job time : 1234.83 secs 210 Ç 210 336 C 336 දු පු

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LENGTH: 480 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1..477
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                       1 ATGTCCGGTTGCTCTTTCTC.....TGATGATGAACTGGTAATAG 480
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Sequence 30,
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Sequence 30,
Sequence 96,
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Sequence 47,
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*
(cgn2_6/ptodata/2/ina/5B_COMB.seq:*
(cgn2_6/ptodata/2/ina/6A_COMB.seq:*
(cgn2_6/ptodata/2/ina/6B_COMB.seq:*
(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-470-426B-14

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US-09-014-416-6

US-09-014-416-6

US-08-612-973-7

US-08-927-597-7

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US-08-927-930

US-08-01-912-30

US-08-01-912-30

US-08-612-973-3

US-08-612-973-3

US-08-612-973-4

US-08-612-973-47

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US-08-612-973-13
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Maximum Match 100%
Listing first 45 summaries
                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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431.2
431.2
428
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Sequence 3, Sequence 3, 1
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Sequence 9,
Sequence 9,
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Sequence 3,
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APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUSKAN, FONS
APPLICANT: BUSKAN, FONS
APPLICANT: BUSKY, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                  Sequence
Sequence
Sequence
Sequence
                                                                                                                                                              Sequence
Sequence
Sequence
                           Sequence
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STREET: 1100 NORTH CITY: ALLINGTON
STRATE: VIRGINA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: EDADA GISK
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25 (EPO)
COMPUTER: PATENTIN NUMBER: US/08/612,973
FILING DATE: II-MAR-1996
CASSIFICATION NUMBER: 3.205
REFERENCE/DOCKET NUMBER: 1487-10
TELEPOMMUNICATION INPORMATION:
TELEPOMMUNICATION INPORMATION:
TELEPOMMUNICATION INPORMATION:
TELEPOMMUNICATION INPORMATION:
TELEPOMMUNICATION INPORMATION:
TELEPOMMUNICATION NUMBER: 148000
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US-08-481-695-28
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US-08-904-686A-9
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Patent No. 6150134
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1167
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Sequence 11, Application US/08927597

Sequence 11, Application US/08927597

Sequence 11, Application US/08927597

Select No. 6245503

APPLICANT: MARRIENS, GERET APPLICANT: BOSMAN, FONS

APPLICANT: BOSMAN, FONS

TITLE OF INVENTION: PROFIED HEPATITIS C VIRUS ENVELOPE

TITLE OF INVENTION: PROFIED HEPATITIS C VIRUS ENVELOPE

TITLE OF INVENTION: PROFIED HEPATITIS C VIRUS ENVELOPE

TITLE OF INVENTION: PROFIED FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE NIXON & VARDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER PAPEINCATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/927,597
                                                                                 1 ATGICCGGITGCICITICICTICICICITIGCCCTGCTGTCCTGTCTGACCAIACCA
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0
                 Length 480;
                                          0; Indels
                  100.0%; Score 480; DB 3; L
100.0%; Pred. No. 7.1e-126;
ive 0; Mismatches 0;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
                         Query Match
Best Local Similarity 100.
Matches 480; Conservative
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US-08-612-973-9

US-08-612-973-9

Sequence 9, Application US/08612973

Sequence 9. Application US/08612973

Patent No. 6150134

GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BUNNEN, FONS
APPLICANT: BUNNEN, MARIE-AND
TITLE OF INVENTION: PROTEINE HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
INVENESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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100.0%; Score 480; DB 3; L
Best Local Similarity 100.0%; Pred. No. 7.1e-126;
Matches 480; Conservative 0; Mismatches 0;
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                             NAME/KEY: mat_peptide
;
! LOCATION: 1..474
US-08-927-597-11
                                                                                                                                                                                                                                                                 1..477
                                                                                                                                                                             MOLECULE TYPE: CDN
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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LOCATION:
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181 TGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCC 240
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                                  Sequence 9, Application US/08927597

Ratent No. 6245503

GENERAL INFORMATION:
GENERAL PROPAGATION:
APPLICANT: BCSWAN, FONS
APPLICANT: BCSWAN, FONS
APPLICANT: BUYEE, WARTHOFF, GUY
APPLICANT: BUYEE, WARTHOFF, GUY
APPLICANT: BUYEE, WARTHOFF, GUY
APPLICANT: BUYEE, MARTHOFF, GUY
APPLICANT: BUYEE, MARTHOFF, GUY
APPLICANT: BUYEE, MARTHOFF, GUY
APPLICANT: BUYEE, MARTHOFF, GUY
APPLICANT: BUYEE, AND THERAPEUTIC USE
UNUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 474.2; DB 3; Length 483; Pred. No. 3e-124; 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                          ZIE: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25 (BPO)
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIPICATION:
CLASSIPICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                      ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.4%;
Matches 476; Conservative 0
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                                                                                                                                                                                                                                                                                                           STREET: 1100 NOR:
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTAATC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GCTGCTTTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGGATCTGTTTTCCTTGTTTCC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 cadcherroaccrococcoccacarcaacagracagacrocaacrocaacrocaarc 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATCCCGGCCATGTATCAGGTCACCGCATGCTTGGGATATGATGAAGAGTAGTAATA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 TATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCCTA 479
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      COUNTRY: U.S.A.
COUNTRY: U.S.A.
COMPUTER RADABLE FORM:
MEDIUT TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DSG/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY THOWAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
MAME: MAME: WANG: NUMBER: 31,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
METERSPONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match

98.8%; Score 474.2; DB 3; Length
Best Local Similarity 99.4%; Pred. No. 3e-124;
Matches 476; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 1..4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , NAME/KEY:
, LOCATION:
US-08-612-973-9
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Sequence 14, Application US/08470426B

Patent No. 5856458
GENERAL INFORMATION:
APPLICANT: Okamoto, Hiroaki
APPLICANT: OLGONUCLEOTIDE PRIMERS, AND THEIR
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-B
TITLE OF INVENTION: HEPATITIS VIRUS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              506 IGCCCGGTIGCICTIICTCIAICTICCICTIGGCTITIGCTGICCTGTITGACCAICCCAG 565
                                                                                                                                                                                                     362 AGCIGITCACCITCICACCICGCCATCAACAGTACAGGACTGCAACTGCTCAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  926 Arcccdaccarriarcadarcacccaragacridacarararararaaraacrdarca 981
                                                            182 gegricegeaagagaaacrecrecegreerregregeerecrecacecrecacecea
                                      ADDRESSEE: Beveridge, DeGrandi, Wellacher & Young, ADDRESSEE: L.L.P.
STREET: 1850 M Street, N.W., Suite 800
CITY: Washington
STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC compatible

OPERATING SYGTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,426B

FILING DATE: 06-JUN-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/470,426B

FILING DATE: 06-JUN-1990

APPLICATION NUMBER: UP 2-153402

FILING DATE: 12-JUN-1990

ATTORNEY/AGENT INFORMATION:

NAME: Weilacher, Robert G.

REGISTRATION NUMBER: 20,531

REGISTRATION NUMBER: 06/59-47083.1

TELEPAN: (202) 659-1462

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1863 base pairs
TYPE: nucleic acid
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US-08-470-426B-14
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Sequence 17, Application US/08470426B
Patent No. 58564508
GENERAL INFORMATION:
APPLICANT: Okamoto, Hiroaki
APPLICANT: Nakamura, Tetauo
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B
TITLE OF INVENTION: HEPATITIS VIRUS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                301 GCrGcrrrcrgrrccacrareracgradagarcrcracagarcrarrrcrarrrccraging
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                                                                                                                                                                                                                  361 CAGCIGITCACCITCICACCICGGGATCAAACAGIACAGGACTGCAACTGCAATC 420
                                                                        300
                                                                                           TATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTAATA 479
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                   241 AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGCT
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IP: 20036

IP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,426B
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: JP 2-153402
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wellacher, Robert G.
REGISTRATION NUMBER: 06/59-47083.1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 17:
SEQUIENCE CHARACTER.ESTICS:
INFORMATION FOR SEQ ID NO: 17:
SEQUIENCE CHARACTER.ESTICS:
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89.8%; Score 431.2; DB 2;
Best Local Similarity 94.1%; Pred. No. 5.1e-112;
Matches 448; Conservative 0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1850 M Street, N.W., Suite 800 CITY: Washington COUNTY: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-470-426B-17
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-470-426B-17
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RESULT 8
US-09-014-416-6

i Sequence 6, Application US/09014416

i Sequence 7. Application US/09014416

j Patent No. 6153421

i GENERAL INFORMATION:

j APPLICANT: Yanaqi, Masayuki

j APPLICANT: Bukh, Jens

j APPLICANT: USBS THEREOF

j TITLE OF INVENTION: USES THEREOF

j TITLE OF INVENTION: USES THEREOF

j CURRENT FILING DATE: 1998-01-27

j EARLIER FILING DATE: 1998-01-27

j EARLIER FILING DATE: 1997-07-18

j NUMBER OF SEQ ID NOS: 65

j SOFTWARE: PATENTIN VET. 2.1

j SEQ ID NO 6
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                                                                                                                                                                                                                                          242 GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG
                                                      907 criccectrargaagrececaacerereceseararacearereaceaeceaeceaecea
                                                                                                                                                                    182 GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCAACGCTCGCGGCCAA
                                                                                                                                                                                                                                                                                                                     CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGGATCTGTTTTCCTTGTTTTCCC
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                                                                                           ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGCGATATGATGATGACTGGTAA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 GCGTTCGGGAGGCCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
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Pred. No. 6.8e-111;
0; Mismatches 30;
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Best Local Similarity 93.7%;
Matches 446; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9599
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Sequence 4, Application US/09014416

Sequence 4, Application US/09014416

Sequence 4, Application US/09014416

GENERAL INFORMATION:

APPLICANT: Bukh, Jens

APPLICANT: Bukh, Jens

APPLICANT: Bukh, Jens

TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 20264276

CURRENT APPLICATION NUMBER: US/09/014,416

CURRENT PILING DATE: 1998-01-27

EARLIER PILING DATE: 1998-01-27

EARLIER PILING DATE: 1997-07-18

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 4

LENGTH: 9595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1190 AGCTGTTCACCTTCTCGCCTCGCCGCATGAGACAGTGCAGGACTGCAACTGCTCAATCT 1249
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                                                                                                                                                                                                                                                           GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG
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                                                                                                                                                                2 TGTCCGGTTGCTCTTTCTCTTTCTTCTTGGCCCTGCTGTCTGTCTGACCATACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTAA 477
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                                                                                           Length 1863;
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Pred. No. 6.8e-111;
0; Mismatches 30; Indels
                                                                                                                           Indels
                                                                                       Score 431.2; DB 2;
Pred. No. 5.4e-112;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TGTCCGGTTGCTCTTTCTTTCTTCCTCTTGGCCCTGC
             ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-470-426B-14
                                                                                     Query Match
Best Local Similarity 94.1%;
Matches 448; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.2%;
93.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 93.7
Matches 446, Conservative
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-09-014-416-4
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242 GGAACGCCAGCGTCCCCACAACGACAATAACGACGCCACGTCGATTTGCTCGTTGGGGCTG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08927597

Sequence 7, Application US/08927597

Patent No. 6245503

GENERAL INFORMATION:
APPLICANT: BENERAL
APPLICANT: BOSMAN, FONS
APPLICANT: APLINGTON
STATE: UIGO NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: UIGO NORTH GLEBE ROAD
CITY: ALLINGTON
STATE: UIGO NORTH GLEBE FORM:
ACOUNTRY: U.S.A.
COMPUTER READABLE FORM:
ACOUNTRY: ALLINGTON
ACOUNTRY: 
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2 igrecognigererricerenterecreterecreergrecretereseas
                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/612,973
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 12,205
REFERENCE/DOCKET NUMBER: 1487-
TELECHOMINICATION INFORMATION:
TELECHOMINICATION 1031 816-4100
TELEFRAX: (703) 816-4100
TELEFRAX: (703) 816-4100
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US-08-927-597-7
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                                GGAACGCCAGGCTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGCTG
                                                                                                                                                 302 cracificatrocarrataracaragasarcracasarcratarificararratrocc
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APPLICANT: MERTENS, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUSE, MARIE-ANGE
TITLE OF INVENTION: PUTIFIED OF DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1100 NORTH GLEBE ROAD
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ZIP: 22201-4714

COUNTY: 0.5.4.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: FORDEN GLEDE #1.0, Version #1.25 (EPO)
SOFTWARE: Patentln Release #1.20 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-08-612-973-7
US-08-612-973-7
Sequence 7, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: HOSMAN, FONS
APPLICANT: HOSMAN, FONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 93.1%;
Matches 446; Conservative
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ANTI-SENSE: NO
FEATURE:
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US-08-612-973-7
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM_FC compatible
OPERATING SYSTEM: PC-DOS/W3-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
FILING DATE: 18-MAR-1993
APPLICATION NUMBER: FR 91 06 882
FILING DATE: 06-JUN-1991
ATORNEY, AGENT INFORMATION:
NAME: Meyers, Kenneth J.
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05286-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 30.
SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.4%;
Matches 439; Conservative
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rus Isolate, Diagnostic and Therapeutic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 GCGTTCGGGAGACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTA 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 426.2; DB 3; Length
Pred. No. 1e-110;
0; Mismatches 33; Indels
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Patent No. 5866139
GENERAL INFORMATION:
APPLICANT: Brechot, Christian
APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Porchon, Coletted and Peptide Sequence
TITLE OF INVENTION: Nucleotide and Peptide Sequence
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diaa;
TITLE OF SEQUENCES:
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 93.1%;
Matches 446; Conservative
                     LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                    mat_peptide
1..627
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                ANTI-SENSE: NO FEATURE:
                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-927-597-7
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US-08-483-695-30
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     Length 501;
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Pred. No. 5.8e-110;
0; Mismatches 26;
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US-07-965-285-30
; Sequence 30, Application US/07965285
; Patent No. 5879904
; GENERAL INFORMATION:
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Sequence 30, Application US/08487231
Sequence 30, Application US/08487231
Sequence 30, Application US/08487231
Sequence 30, Application:
APPLICANT: Brechor, Christian
APPLICANT: Porchon, Colette
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleocide and Peptide Sequences of a TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic TITLE OF INVENTION: Applications
NUMBER OP SEQUENCES: 46
CORRESPONDENCE ADDRESS: 4
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner ADDRESSEE
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llarity 94.4%; Pred. No. 5.8e-110;
Conservative 0; Mismatches 26;
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STATE: MASHINGSON
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1..
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,231
FILING DATE: 07-UUNE-1995
CLASSIFICATION DATA:
APPLICATION WOWABER: US 07/965,285
FILING DATE: 18-MAR-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: R8 91 06 882
FILING DATE: 06-UUN-1991
ATTORNEY/AGENT INFORMATION
NAME: MSYSTEM INFORMATION:
NAME: MSYSTEM INFORMATION:
REGISTRATION NUMBER: E3 25,146
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05286-0001-02000
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 30:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS LENGTH: 501 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202-408-4400
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Best Local Similarity
Matches 439; Conserv
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                          APPLICANT: Brechot, Christian
APPLICANT: Kremsdorf, Dina
APPLICANT: Rochon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
MINMER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 rececedirecrerrerrerrerrecrerrescerrischerecrerrisacearecade 96
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88.2%; Score 423.4; DB 2; Length 501;
Best Local Similarity 94.4%; Pred. No. 5.8e-110;
Matches 439; Conservative 0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopped disk

COMPOTER: IBM PC compatible

COMPOTER: IBM PC compatible

COMPOTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

ENGRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/965,285

PRIOR APPLICATION NUMBER: FF 91 06 882

PLING DATE: 06-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAMME: MCYCKET WUMBER: 05286-0001-00000

TELERPAN: 202-408-4400

TELERPAN: 202-408-4400

TELERPAN: 202-408-4400
                                                                                                                                                                                                                                                              ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
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SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
DESCRIPTION: CDNA to genomic RNA
                                                                                                                                                                                                                                                                                                                 STREET: 1300 I Street, N.W. CITY: Washington STATE: DC
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                                                                                                                   37 JGCCCGGTTGCTCTTTCTCTTTCTTCTCTCTTGCTTTGCTGTTTGACCATCCAG
                                                                                                                                                                                                     GCGTTCGGGAGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
COMPUTER: IBM PC/Dentium
COMPUTER: IBM PC/Dentium
COMPUTER: IBM PC/Dentium
COMPERATING SYSTEM: Windows
SOFTWARE: Microsoft Word
CURRENT APPLICATION NUMBER: US/08/150,204E
FILING DATE: 20-Apr-1994
CLASSIFICATION NUMBER: US/08/150,204E
FILING DATE: 20-Apr-1994
FRIOR APPLICATION DATA:
RAPPLICATION NUMBER: KR 91-9510
FILING DATE: 10-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 ATCCCGGCCATITATCAGGTCACCGCATGGCTTGGGATATGATGA 501
                                           Indels
Score 423.4; DB 3;
Pred. No. 5.8e-110;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: YANG, Jae Young
STREET: 386-1, Doryong-dong, Yuseong-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-150-204E-96
; Sequence 96, Application US/08150204E
; Patent No. 6538126
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHO, Joong Myung
LEE, Yong Beom
PARK, Young Woo
LIM, Kook Jin
CHOI, Deog Young
SO, Hong Seob
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KIM, Sung Taek
YANG, Jae Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 128
Query Match
Best Local Similarity 94.4%;
Matches 439; Conservative
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Patent No. 6210962
GENERAL INFORMATION:
APPLICANT: Brechot, Christian
APPLICANT: Kremsdorf, Dina
APPLICANT: Forchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C virus Isolate, Diagnostic and Therapeutic
TITLE OF SEQUENCES: 46
                                                                                      217 GCGTTCGGGAGACAACAGCTCCCGTTGCTGGGTAGCGCTCACCCTCCCACGCTCGCGGCA 276
                                                                                                                                                                        CIGCTITICIGITICCGCTAIGTACGIGGGGAICTCTGCGGAICTGITITICCTTGITITCCC 361
                                                                                                                                                 GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG 301
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ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
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ZIP: 20005-3315
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,912
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,285
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05286-0001-00000
TELEPONMULCATION INFORMATION:
TELEPHONE: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA to genomic RNA
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TYPE: nucleic acid
STRANDEDNESS: single
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DESCRIPTION:
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Best Local Similarity 93.2%; Pred. No. 2e-109;
Matches 442; Conservative 0; Mismatches 32; Indels
                                                                                                                                                                                  ); SEQUENCE DESCRIPTION: KHCV-LBC1, Fig. 2
; SEQUENCE DESCRIPTION: SEQ ID NO: 96
US-08-150-204E-96
APPLICATION NUMBER: KR 91-13601
FILING DATE: 6-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Shahan Islam, ESQ.
REGISTRATION NUMBER: 26-55/FLK
REPERBUCE/DOCKET NUMBER: 26-55/FLK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 940-8564
TELEFAX: (212) 940-876
INFORMATION FOR SEQ ID NO: 96
SEQUENCE CHARACTERISTICS:
LENGTH: 9472 base pairs
TYPE: nucleic acid
STRANDENNES: double
TYPE: nucleic acid
STRANDENNES: double
TYPE: TYPE: DASE
MOLECULE TYPE: DNA
FEATURE:
FEATURE:
OFFICE TAPE: DNA
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Search completed: December 20, 2003, 07:03:01 Job time : 35.6174 secs

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December 19, 2003, 16:55:48; Search time 2408.07 Seconds (without alignments) 10804.703 Million cell updates/sec
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1 ATGCTGGGTAAGGCCATCGA.....TGATGAACTGGTACTAATAG 636
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | A48675 Sequence AX457129 Sequence AX457129 Sequence AX452762 Sequence AX685014 Sequence AX685018 Sequence AX452756 Sequence AX452756 Sequence AX452756 Sequence AX452756 Sequence AX452759 Sequence AX457754 Sequence AX457759 Sequence AX45775 Sequence AX45779 Sequence AX45779 Sequence AX68505 Sequence AX68505 Sequence AX68505 Hepatitis AF16505 CDNA encodi B04805 CDNA Sequence AX03652 Sequence | linear PAT 07-MAR-1997 e,M. EINS FOR DIAGNOSTIC AND |
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| OI . | A48675 AA157329 AX685014 AA8669 AX685014 AA8669 AX7851326 AX78508 AA6667 AX785008 AA667 AX752754 AX685006 AX752735 AX752736 AX73273 AX73373 AX733971 AX733971 AX733971 AX7336260 | 636 bp DNA li tent W09604385. 18 C. Y. P., M.G. and Buyse, M. C. VIRUS ENVELOPE PROTEINS |
| % Query Match Length DB | 00000000000000000000000000000000000000 | A48675 Sequence 13 from Patent A48675 A48675.1 GI:2302388 unidentified unclassified. 1 (bases 1 to 636) Maertens,G., Bosman,F., PURLFIED HEPATITIS C VI THERAPEUTIC USE PATENT WO 9604385-A 13 |
| Result No. Score | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | RESULT 1 A48675 LOCUS LOCUS ACCESSION A4 VERSION A4 TITLE TH JOURNAL PP |

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llarity 100.0%; Pred. No. 5.5e-137;
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                 INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 382495 960304.
Location/Qualifiers
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Purified Hepatitis C Virus envelope proteins for diagnostic therapeutic use
Patent: WO 02055548-A 13 18-JUL-2002;
INNOGENETICS N.V. (BE)
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                                TCCGGGATGTACCATGTCACGACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
                                               GACATGATCATGCACACCCCGGGTGCGTGCCTGCGTTCGGGAGAACAACTCTTCCCGC
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Maertens, G., Bosman, F., De, M.G. and Buyse, M.
Maertens, G., Bosman, F., De, M.G. and Buyse, M.
THERAPEUTIC USE
PARENTIC USE
PARENT: WO 9604385-A 7 15-FEB-1996;
INNOGENETICS NV (BE)
Other publication CA 217273 960215
Other publication AU 382495 960304.
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IMHTPGCVPCVRENNSSRGWVALTPTLAARNAVPTTTIRHVDL.VGAAAFCSAMYV
GDLCGSVFLVSQLFTISPRRHETVQDCNCSIYPGHITGHRMAWDMMMN"
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/mol_type="genomic DNA"
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VNATGRULGGCSFSIFLLAGCLTIPRAYEVRINSGWYTYRDCSNSSIVYERADM
IMHTPGCVPCVRENSSRCWWLTPTLAARNSVPTTTIRRHVDL.VGAAAFCSAMYV
GDLCGSVFLVSQLFTISPRRHETVQDCNCSIYPGHITGHRMAMDMMMN"
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    /note="unnamed protein product"

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/mol_type="genomic DNA"
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QLIRIPGAVVDWVAGAHWGVLAGLAYYSMVGNWAKVLIVMLLFAP"
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'db_xref="taxon:32644"
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Location/Qualifiers

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Jorganism="unidentified"
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 Maertens, G., Bosman, F., de Martynoff, G. and Buyse, M.A. Recombinant vectors for producing how envelope proteins Patent: BP 1211315-A 5 05-JUN-2002; Innogenetics N.V. (BE)
Location/Qualifiers
1. 795
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/mol_type="genomic DNA"
/db_xref="taxon:11103"
1. 792
/note="unnamed protein product"
/codon_start=1
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Pred. No. 1.4e-129;
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               Unclassified.

1 (bases 1 to 795)
Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic
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Pred. No. 1.4e-129;
0; Mismatches 15;
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Hepatitis C virus
Viruses, ssRNA positive-strand viruses,
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Patent: US 6245503-A 5 12-JUN-2001;
Location/Qualifiers
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Sequence 5 from Patent EP1211315.
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Purified Hepatitis C Virus envelope proteins for diagnostic
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Pred. No. 1.4e-129;
0; Mismatches 15;
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1. 792
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                                                                                           Viruses; BSRNA positive-strand viruses,
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Patent: WO 02055548-A 5 18-JUL-2002;
INNOGENETICS N.V. (BE)
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/product="unnamed"
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                             541 CATGAGAGGGGGGGAGTGCAATTGCTCAATCTGTCGGGCCACATAAGGGGTCACGT
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/note="unnamed protein product"
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IFKVRMYVGGVEHRFEAACMYTRGBRCDLEDRDRSELSPLLLLSTTEWOILPCSFTTLP
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AQARAALENLVVLNAAAVAGAHGTLSFLVFFCAAWYIKGRLVPGAAYAFYGVWPLLLL
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SDTRGLVSLFSPGSAQKI QLVNTNGSWHINRTALNCNDSLQTGFFAALFYKHKFNSSG
CPERLASCRSIDKFAQGWGPLTYTEPNSSDQRPYCWHYAPRPCGI VPASQVCGPVYCF
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Maertens,G., Bosman,F., de Martynoff,G. and Buyse,M.A.
Recombinant vectors for producing hov envelope proteins
Patent: EP 1211315-A 47 05-JUN-2002;
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AX422796 GI:21712481
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Unclassified.
1 (bases 1 to 2082)
Maertens,G., Bosman,F., De Martynoff,G. and Buyse,M.-A..
Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use 245503-A 47 12-UUN-2001;
Patent: US 6245503-A 47 12-UUN-2001;
GACGCCACGTCGATTTGCTCGTTGGGGGGGCTGCTTTCTGTTCCGCTATGTACGTGGGGG
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HCV, E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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                                                             Bosman F, Buyse M,
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Hepatific C virus
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1 cand E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. C in vectors for the production of recombinant E1, E2, and E1/E2 proteins. C invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a correspond cleavage agent, after 1918 of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated by known are reactive with human sera than those isolated by known
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produce proteins suitable for direct use in vaccines or diagnostic
assays of HCV
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                                                                                                                                                                                                              Claim 23; Fig 21; 146pp; English
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV) specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or B2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for the vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.

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Gaps

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Length Indels

100.0%; Score 636; DB 24; 100.0%; Pred. No. 7.2e-162; iive 0; Mismatches 0;

Query Match 100. Best Local Similarity 100. Matches 636; Conservative

Sequence 636 BP; 111 A; 197 C; 175 G; 153 T; 0 other;

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1 ATGCTGGGTAAGGCCATCGATACCCTTACGTGCGGCTTCGCCGACCTCGTGGGGGTACATT CCGCTCGTCGCCCCCTAAGGGGGCCCTGCCAAGGGCCCTGGCGCATGGCGTTCGGGGTT

120 120 180 CTGGAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTC 180 CTCTTGGCTTTACTGTCCTGTCTAACCATTCCAGCTTCCGGCTACGAGGTGCGCAACGTG 240

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New therapeutic vaccine compositions comprising at least one purifie recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
                                                                                                              E2 protein; infection; gene; ds.
                                                                                             protein coding sequence.
ATGGCTTGGGATATGATGATGAACTGGTACTAATAG 636
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                                                                                                                 Hepatitis C virus; HCV; B1 protein; virucide; immunostimulant; vaccine;
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                                                                                                Hepatitis C virus clone HCCI17A
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30-AUG-2001; 2001US-315768P.
                                              DNA; 636
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                                                                                                                                                                                                                                            (INNO-) INNOGENETICS NV
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                                                                                                                                                                                                                                                                                                                                   from HCV infection
                                              AAL48918 standard;
                                                                                                                                            Hepatitis C virus.
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P-PSDB; AAO18665.
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serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                               241 TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTGTATGAGGGAGCG
                                                                    GGGGATCTCTGCGGATCTGTCTTCCTCGCCCAGCTGTTCACCATCTCGCCTCGCCGG
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                   TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
                                                         GACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGC
                                                                                                TGCTGGGTAGCGCTCACCCCCACGCTCGCGGCTAGGAACGCCAGCATCCCCACTACAACA
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins: The recombinant proteins can then be isolated using a method of the

Claim 23; Fig 21; 146pp; English.

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invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known
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                                                                                                                                                                                                                                                                                                                                             New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein B1 or B2, useful for immunizing humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                 Hepatitis C virus; HCV; El protein; E2 protein; infection; gene; virucide; immunostimulant; vaccine; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

96.4%; Score 612.8; DB 24; Length 633;
Best Local Similarity 98.1%; Pred. No. 1.3e-155;
Matches 620; Conservative 0; Mismatches 12; Indels 0;
      Hepatitis C virus clone HCCI11A El protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 633 BP; 111 A; 192 C; 174 G; 156 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 163-164; 243pp; English.
                                                                                                                                                                                                                                                                              Buyse M;
                                                                                                                                                                                                    11-JAN-2001; 2001US-260699P.
30-AUG-2001; 2001US-315768P.
                                                                                                                                                                         11-JAN-2002; 2002WO-EP00219.
                                                                                                                                                                                                                                                   (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                               Bosman F,
                                                                                                                                                                                                                                                                                                          WPI; 2002-599657/64.
P-PSDB; AAO18662.
                                                                                                                                                                                                                                                                                                                                                                                                  from HCV infection
                                                                                 Hepatitis C virus.
                                                                                                                  WO200255548-A2.
                                                                                                                                                                                                                                                                                   Maertens G,
                                                                                                                                                18-JUL-2002
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AMTI2704-T12709 and AATI2961-T12974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant El, E2, and El/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by a carrying out a disulphide bond cleavage, or a reduction step with a crarying out a disulphide bond cleavage, or a reduction step with a crarying out a disulphide bond cleavage, or a reduction step with a crarying out a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for antibodies in a sample, and in a serctyping assay for detecting one or antibodies in a sample, and in a serctyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the
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                                  ATACGACGCCACGTCGATTTGGTTGGTTGGGGGGGGCTGCTTTCTGTTTCCGCTATGTACGTG
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                                                                                                                                                                                                                                                                                                                       CATGAGACGGTGCAGGACTGCAATTGCTATCTATCCGGGCCACATAACGGGTCACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 23; Fig 21; 146pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT12705 standard; DNA; 795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCV E1 construct HCCI10A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-1995;
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inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or B2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 GGGGATCTCTGCGGATCTGTCTTCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGG 540
                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to new therapeutic vaccine compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of patients suffering from HCV infection. The present sequen
is a coding sequence described in the exemplification of the invention
                                                                                                                                                                                                                                                    New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
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Pred. No. 3.3e-153;
0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                               2; Page 161-162; 243pp; English.
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Local Similarity 97.6%;
Nes 613; Conservative (
                                                                        11-JAN-2001; 2001US-260699P. 30-AUG-2001; 2001US-315768P.
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P-PSDB; AAO18661.
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                                         11-JAN-2002;
       18-JUL-2002
                                                                                                                                                                Maertens G,
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conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known
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                                                                                                                                                              Gaps
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                                                                                                                                                              .
0
                                                                                                                       Score 604; DB 17; Length 795;
Pred. No. 3.3e-153;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus clone HCCI10A El protein coding sequence
                                                                                       BP; 130 A; 240 C; 231 G; 194 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               628
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virucide; immunostimulant; vaccine;
                                                                                                                         95.0%;
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                                                                                                                                                          613; Conservative
                                                                                                                                      Best Local Similarity
Matches 613; Conserv
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                                                                                       Sequence 795
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HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545 AGACGGTGCAAGACTGCAATTGCTCAATCTATCCAGACAAAAAGGGGTCACGTATGG
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                                                                                                                                                                                                                                                                                                                                                                                                           TGATCATGCACACCCCCGGGGTGCGTGCCTGCGTTCGGGAAGAACAACTTTCCCCGCTGCT
        65 TCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGG
                                                                                                                 TGGCTTTACTGTCCTGTCTAACCATTCCAGCTTCCGGCTTACGAGGTGCGCAACGTGTCCG
                                                                                                                                                                                                                                   125 AAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTCT
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proteins - in presence of di:sulphide bond cleavage agent, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein B1 or B2, useful for immunizing humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
  CATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACGT
                                                                                                               Query Match 94.6%; Score 601.6; DB 24; Length 2082; Best Local Similarity 97.8%; Pred. No. 2e-152; Matches 610; Conservative 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; El protein; E2 protein; infection; gene; virucide; immunostimulant; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus E2 protein related coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2082 BP; 366 A; 634 C; 600 G; 482 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 206-209; 243pp; English.
                                                                                                                                                                                                                                   601 ATGGCTTGGGATATGATGATGAACTGGT 628
                                                                                                                                                                                                       ATGGCTTGGGATATGATGATGAACTGGT 628
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30-AUG-2001; 2001US-315768P.
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1
and E2 protein coding sequence constructs. These sequences are included
in vectors for the production of recombinant E1, E2, and E1/E2 proteins.
The recombinant proteins can then be isolated using a method of the
invention. In the method, the envelope proteins are purified by
carrying out a disulphide bond cleavage, or a reduction step with a
disulphide bond cleavage agent, after lysis of recombinant host cells.
The constructs containing the purified HCV envelope proteins can be used
for vaccinating humans against HCV, for in vitro detecting one or
antibodies in a sample, and in a seroctyping assay for detecting one or
more serological types of HCV present in a biological sample. The
constructs can also be immobilised on a solid substrate and incorporated
into a reversed phase hybridisation assay for determining the presence or
the genotype of HCV. The new purification method preserves the
conformation of the recombinantly expressed E1, E2 and E1/E2, and
are more rearried man are a than those isolated using this method
are more rearried with human ears than those isolated wing this method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
produce proteins suitable for direct use, in vaccines or diagnostic assays of {\sf HCV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 601.6; DB 17; Length 2086;
Pred. No. 2e-152;
0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                           more reactive with human sera than those isolated by known
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2086 BP; 366 A; 635 C; 601 G; 484 T; 0 other;
                                                                 Claim 23; Fig 21; 146pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.8%;
Matches 610; Conservative (
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and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent, after lysis of recombinant host calls. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 AAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTCT 184
                                                                                                                                                                                                HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 TCGTCGGCCCCCCTAGGGGGCCCTGCCAGGCCCTGGCGATGCGGGTTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of dissulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 601.6; DB 17; Length 2433;
Pred. No. 2.1e-152;
0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2433 BP; 434 A; 745 C; 714 G; 540 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De Martynoff G, Maertens G;
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                                       AAT12974 standard; DNA; 2433 BP
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Best Local Similarity 97.8%;
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                                                                                                                                                                                                                                                                              Hepatitis C virus.
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV El and/or E2 proteins are useful as against HCV. The recombinant HCV screening and confirmatory antibody vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                                                                                                                                                   Sequence 2434 BP; 434 A; 745 C; 714 G; 541 T; 0 other;
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                                                             TGGCTTTACTGTCCTGTCTAACCATTCCAGCTTACGAGGTGCGCAACGTGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus E2 protein related coding sequence SEQ ID NO: 49.
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30-AUG-2001; 2001US-315768P.
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P-PSDB; AAO18679.
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                                                                 361 GTAGCGCTCACCCCCACGCTTGCGGCCAGGAACGCTAGCGTCCCTACTACGACATACGA
                                                                                                           427 GGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGGGAT
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                          GTAGCGCTCACCCCCACGCTCGCGGCTAGGAACGCCAGCATCCCCCACTACAATACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cuticle protein 1 and 2 secreting hepatitis C virus (Japanese)
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                                                                                                                                                                                                                                                                                                                                                                                               601 TGGGATATGATGATGAACTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This nucleotide comprises the hepatitis C virus (HCV) cDNA insert in plasmid pA10. This cDNA was obtained by PCR amplification of HCV conds using primers (see AAV38849-50) designed to amplify the HCV core gene. The PCR product was cloned into pBluescript KS to create pA10. It encodes a 224-amino acid polypeptide (see AAW62825). The HCV core protein can be used as an immunogen in novel fusion proteins (see AAW62657-59) that comprise HCV core protein and at least 19 amino acids (see AAW62827) of the C terminal sequence of the large protein from hepatitis D virus (L-HDAg). In novel virus-like partials of the invention, a fusion protein immunogen is at least partially enveloped by hepatitis B surface antigen. The virus-like particle is used to ameliorate or protect against infections caused by hepatitis B virus and/or another microorganism, especially HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTAAGGCCATCGATACCCTTACGTGCGGCTTCGCCGACCTCGTGGGGTACATTCCGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virus-like particle for, e.g. treating microbial infection - comprises polypeptide from microorganism and sequence from Hepatitis D virus large protein, partially enveloped by Hepatitis B surface antigen
                                   HBC; core protein; hepatitis D virus; L-HDAg; virus-like particle; infection; hepatitis B virus surface antigen; HBsAg; immunogen; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 561.2; DB 19; Length 673;
Pred. No. 1.1e-141;
0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 673 BP; 115 A; 208 C; 188 G; 162 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           (QUEE-) QUEENSLAND DEPT HEALTH SAKZEWSKI VIRUS.
protein cDNA insert of plasmid pA10.
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Best Local Similarity 93.9%;
Matches 584; Conservative
                                                                                                                                                                                                                                                        97WO-AU00884
                                                                                                                                                                                                                                                                                                     96AU-0004341
                                                                                                                                                                                                                                                                                                                                                                                          MacNaughton TB,
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P-PSDB; AAW62825.
                                                                                                                             Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGTAAGGCCATCGATACCCTTACGTGCGGCTTCGCCGACCTCGTGGGGTACATTCCGC
                                                                                                                                                                                                                                   The sequence is that of NANB hepatitis virus polynucleotide N-2540-2 which codes for a non-A, non-B (NANB) hepatitis virus gene HC-CM. The polypeptide it encodes may be used in a system for detecting NANB hepatitis. This method is highly specific and sensitive, and can detect NANB hepatitis virus which could not be detected by conventional methods.
                                                                                                                    Antigen related to non-A and non-B hepatitis virus - comprises non-translation region comprising 340 - 341 mols. of nucleotides, non-translation region comprising 1885 - 2551 mols. of nucleotides including region 1,149 and, etc.
                                                                                                                                                                                                                                                                                                                                                                                      Score 556.8; DB 14; Length
Pred. No. 2.7e-140;
0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                        Sequence 2540 BP; 471 A; 775 C; 741 G; 553 T; 0 other;
                                                                                                                                                                                                             Claim 3; Page 19-20; 73pp; Japanese.
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Best Local Similarity 93.3%;
Matches 582; Conservative
90JP-0153401
90JP-0304405
                                                                                WPI; 1993-199637/25.
P-PSDB; AAR38279.
                                                 (NAKA/) NAKAMURA T
 12-JUN-1990;
08-NOV-1990;
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                                                                                           TGGGTAAGGCCATCGATACCCTTACGTGCGGCTTCGCCGACCTCGTGGGGTACATTCCGC
                          terminal of NANBH virus RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-A, non-B; virus; polymerase chain reaction; sensitive; specific; HCV; NANBH; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NANB hepatitis virus polynucleotide N-2540-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication
                                                                                                          1117 dacidecencia de la contración de la
                                                                                                                                                                                                                                                                                                  545 AGACGGTGCAGGACTGCAATTGCTCAATCTATCCGGGCCACATAACGGGTCACCGTATGG
                                                                                                                                                                      ATCTCTGCGGATCTGCCTCGTCTCCCCAGCTGTTCACCATCTCGCCTCGCCGGCATG
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/*tag= a
/prodet= "HCV polyprotein"
/note= "The polyprotein consists of the Core, E1,
E2, P7, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HCV; ds; Con 1; adaptive mutation; liver failure; cirrhosis;
hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
internal ribosome entry site; IRES; NS5A; HCV replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus Con 1 isolate DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-2001; 2001US-263479P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAQ63752-53 represent fragments of the non-A, non-B hepatitis virus (NANBHV) genome. These fragments were amplified using the primers given in AAQ63732-51. These primers were used in the detection of NANBH. The primers are based on the 5'-terminal region and the core protein coding region. The method allows highly sensitive detection of NANBHV.
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                                                                                                                                                                                                                                                                                                                   Polymerase chain reaction; PCR; primer; amplify; detection; NANBHV; non-B hepatitis virus; 5'-terminal region; core protein; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonuclectide primer pairs specific for non-A, non-B hepatitis virus - used for high sensitivity detection of non-A non-B (NANB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 556.8; DB 15; Length 2540;
Pred. No. 2.7e-140;
0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2540 BP; 470 A; 775 C; 742 G; 553 T; 0 other;
                                                                         ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 24-25; 25pp; Japanese.
                                                                  AAQ63753 standard; cDNA to mRNA; 2540
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93.3%;
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                                                                                                                                                                                                                                                       NANBHV genomic fragment #2
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1es 582; Conservative
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RESULT 14
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HCV (hepatitis C virus) replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful instruction HCV replicon, and HCV and host cell interactions, producing HCV RAA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is the HCV replicon Con 1, used as a basis for the adaptive mutations of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGACA 304
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                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                               Query Match
Best Local Similarity 93.3%; pred. No. 4e-140;
Matches 582; Conservative 0; Mismatches 42; Indels 0;
                                                                                                                                                                       Sequence 9605 BP; 1910 A; 2883 C; 2733 G; 2079 T; 0 other;
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EX460099 BX460099
CC40010084 PUBCJ72TB
CC40010084 PUBCJ72TB
CC405167 PUBCST7TD
CC359028 PUBCJ71BTD
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AV635812 AV638281
AV635811 AV632811
AV632335 AV63355
AV63185 AV63185

Sequence:

Run on:

Searched:

Database

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)

1 (bases 1 to 488)

2 (au, 7. Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H., Gu, Y., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, Y., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gao, G., Wang, Z., Zhang, Q., Chen, S., Han, Z. and Chen, Z. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
151 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801912
Fax: 86-21-50801912
Fax: 6-21-50801912
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         AV755731 AV755731 BM Homo sapiens CDNA clone BMFAKB03 5', mRNA sequence.
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                                   CNS0091P
BJ252669
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CC010084
CC405164
BZ736582
CC359028
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CC010085
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AV639521
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AV639153
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AV637643
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ACCESSION
VERSION
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SOURCE
ORGANISM
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LOCUS
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AV755731 AV755731
AV758366 AV758366
BX356664 BX356664
CD040840 psHB036xB
                                                        December 19, 2003, 18:03:34; Search time 1636.15 Seconds (without alignments) 9447.586 Million cell updates/sec
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1 ATGCTGGGTAAGGCCATCGA.....TGATGAACTGGTACTAATAG 636
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      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                            22781392 segs, 12152238056 residues
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        nucleic search, using sw model
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AV758366
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Maximum DB seq length: 2000000000
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BE337089 894043G08 BI723733 1031067F0 AV639153 AV639153 AV638474 AV638474

AL341675 Tetraodon

EST 19-OCT-2000

So. Result

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1 (bases 1 to 492)

1 (bases 1 to 492)

2 (b., '. Zhao, M., Hung, O., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H., Cay, Y., Li, N., Olan, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, Ch., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gao, G., Wang, Z., Zhang, Q., Chen, S., Han, Z. and Chen, Z. Unpublished
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Contact: Zeguang Han
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Contact: Zeguang Han
Sist Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzagechgc: 8h.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
125 g 112 t 3 others
                                                                                                           /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM35.8"
/clone_lib="BM35.8"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
/note="Vector: pTriplEx2; Site_1 4 others
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                                                                                                                                                                                                                                                                                                                              Length 488;
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                                                                                                                                                                                                                                                                                                                              Score 75.4; DB 9;
Pred. No. 3.6e-09;
0; Mismatches 51;
organism="Homo sapiens"
                          /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                   /clone="BMFAKB03"
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Best Local Similarity 70.3%;
Matches 130; Conservative
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Homo sapiens
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/clone lib="Home sapiens PLACENIA COT 25-NORMALIZED"
/clone lib="Home sapiens PLACENIA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a Not1-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
88 c 93 g 398 t 506 others
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1 (bases 1 to 1201)

1 (bases 2 to 1201)

1 (bases 3 to 1201)

1 (bases 1 to 1201)

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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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6.6%; Score 42; DB 13; Length 1201;
Best Local Similarity 10.7%; Pred. No. 2.6; 23; Indels
Matches 57; Conservative 245; Mismatches 232; Indels
Length 492,
                                                                                              50; Indels
Score 61; DB 9; 1
Pred. No. 2.1e-05;
0; Mismatches 50;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIOLYSR03"
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Matches 150; Conservative
   128; Conservative
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Tyler, B.M., Judelson, H.S., Gijzen, M., Dean, R.A. and Waugh, M.E.
USDA-IFAFS: Expression of Phytophthora sojae genes during infection
                                                                                                                                           965 SBSSSSSSSSTTERSTITITYTSSBTTTTSSBTTTTSSTTTTSSTBSSSBSSSSSS 1024
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/cell_line="P6497"
/dev_stage="48 hour post infection"
/clone_lib="psHB: Infected hypocotyl soybean host. 48 hrs
post infection"
                                                                               383 CGCTCGCGGCTAGGAACGCCAGCATCCCCACTACAACAATACGACGCCACGTCGATTTGC 442
                                                                                                                                                                                                                                                        443 TCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCT 502
203 TAACCATTCCAGCTTCCGCTTACGAGGTGCGCAACGTGTCCGGGGATGTACCATGTCACGA 262
                               904
                                                           263 ACGACTGCTCCAACTCCAAGCATTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCG 322
                                                                                                                         GGTGCGTGCCTGCGTTCGGGAGACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                   CD040840 534 bp mRNA linear EST 09-MAY-200 psHB036xB09f_300663 psHB: Infected hypocotyl soybean host. 48 hrs post infection Phytophthora sojae cDNA clone sHB036B09 5, mRNA
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USDA-IFAFS:Expression of Phytophthora sojae genes during
                            845 SSTWTTBISCTSSTINTISSYSSBSISTBSISSTBSSWSBBITTISBISTBTTTISSSS
                                                                                                                                                                                                                                                                                                                                        503 TCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGG 556
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Phytophthora.
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Pred. No. 2.6;
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Tel: 540-231-7318
Email: bmtyler@vt.edu
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/organism="Phytophthora sojae"
/mol_type="mRNA"
/db xref="texon:67593"
/clone="sHB036B09"
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187 c 159 g 87 t
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Seg primer: BK reverse
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Phytophthora sojae
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602834809F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4989195 5',
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (Dases 1 to 1270)
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/clone="IMAGE:4999195"
/lab_host="DH10B (TI phage-resistant)"
/clone lib="WICI CGAP CG24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d:
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 387 c 445 g 164 t
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov.
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov a column: 04
High quality sequence steart: 6
High quality sequence step: 416.
                                                      200 TACGGCGTGCGCGAGATTTACGGTATCCGCATGGGCTTCGCCGGCTTCTACAACTGGACC
                                                                                                                                                                                                                                                                                         343 GAGAACAACTCTTCCCGCTGCTAGCGCTCACCCCCCACGCTCGCGGCTAGGAACGCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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45.3%; Pred. No. 3.8;
tive 0; Mismatches 181;
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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BX3191961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI072YF05 3-PRIME, mRNA sequence.
BX381961
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//db xref="teaxon:5606"
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone="Lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone="lib="Strand cDNA was primed with a NotI-oligo(dT)
/note="list strand cDNA was primed with a NotI-oligo(dT)
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR
aites of the pCNVSPORT 6 vector. Library was normalized.

191 c 115 g 55 t 745 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fullangth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO72CC03NP1.
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ilarity 3.3%; Pred. No. 4.8;
Conservative 189; Mismatches 369; Indels
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/cell_type="T CELLS" (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_tine="JURKAT"
/cell_tine="JURKAT"
/cell_tine="JURKAT"
/cell_tine="Jurkat"
/clone_line="Jurkat"
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/clone_line="Jurkat"
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1 (bases 1 to 1097)

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1 (bases 1 to 1097)

1 (bases 2 to 1097)

1 (bases 2 to 1097)

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2 (bases 2 to 1097)
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cgi-bin/cluster.cgi?seq=CSODJ001AF09NP1&cluster=874.r. Contact
Feng Liang Email: filang@lifetech.com URL
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://Avenue Genoscope sequence ID: CSODJ001AF09NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           390 GGCTAGGAACGCCAGCATCCCCACTACAACAATACGACGCCACGTCGATTTGCTCGTTGG
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850 KNYMYVKGKOKKGKWKKKWKKKWKKKMGKKGBKWCMVKNYMMMMGKGCKWGGKWMMMM
                                                                               270 CTCCAACTCAAGCATTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT
                                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was esquence belongs to sequence cluster 874.r.
more information about this cluster, see
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/clone="CS0DJ001YK17"
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Query Match
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/cione lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotL-ollgo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
194 others
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                                                                                                                                                                                                                                                                                                                                                                                                                         936 AAAMMITAADKIKAAIDIAKDKANIAKHNMNIAMMMKIKKKKWMIMKNIMDKKIKKKK 877
/note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. I 138 c 156 g 178 t 355 others
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Catarrhini, Hominidae, Homo.
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4924.f For
more information about this cluster, see
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cgi.bin/cluster.cgi?seq=CLOBA006ZG08RP1&cluster=4924.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA006ZG08RP1.
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Mammalia; Eutheria; Primates; Catarrhini; Hon
11 (bases 1 to 1201)
11 (M.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
                                                                                                                                        6.4%; Score 40.4; DE 14.3%; Pred. No. 6.7; tive 99; Mismatches
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be 13 ylovo boxin cueux. - KKANUE (E-mall: seqret@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecost digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
                                                                                                                                                                     981 TAAWGGGTAKCVAKCCCMCCCCCAMGCTSGACSCSCCGCAADAAVCGAGMDSGAMKGSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      801 TWGAGGGGGCCCCYCSCMCCCCCCYBBBCCCMCHCTKCSCKMCCRGACTYCCCCASS
                                                                                                                            3 GCTGGGTAAGGCCATCGATACCTTACGTGCGGCTTCGCCGACCTCGTGGGGTACATTCC
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 ACGACGCCACGTCGATTTGCTCGTTGGGGGGGGCTGCTTTCTGTTCCGC 470
   Length 1201;
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DB 9;
6.3%; Score 40.2; DI 26.9%; Pred. No. 7.7;
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/clone="whf25g19"
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1 (bases 1 to 359)

Ogihara, Y. and Murai, K.

Unpublished
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                                                                                                                                                                                                                                                                                                                                     TCTTGGCTTTACTGTCTGTCTAACCATTCCAGCTTCCGCTTACGAGGTGCGCAACGTGT 241
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BJ252669 Y. Ogihara unpublished cDNA library, Wh_f Triticum
aestivum cDNA clone whf25919 3', mRNA sequence.
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                                                                                                                                  Length 925;
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1 Similarity 12.1%; Pred. No. 10;
45; Conservative 164; Mismatches 163; Indels
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                    /...cganism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref="texon:7227"
/clone="BACR19D16"
/clone="lb="RPCI-98"
/note="end: TET3"
/note="end: TET3"
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Triticum aestivum
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SSGSGSGSGSVS 924
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Best Local Similarity
Matches 45; Conserv
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1 (bases 1 to 375)
Ogihara, Y. and Murai, K.
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/tissue_type="spike at flowering date"
/dev stage="Feekes' scale 10.5.1"
/clone lib="Y. Ogihara unpublished cDNA library, Wh_f"
115 c 107 g 67 t
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BJ246716 Y. Ogihara unpublished cDNA library, Wh_f Triticum
aestivum cDNA clone whf25g19 5', mRNA sequence.
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/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxno:4565"
/clone="whf2549"
/tissue_type="spike at flowering date"
/tissue_type="spike at flowering date"
/dev_stage="Reekes' scale 10.5.1"
/clone_lib="Y. Ogihara unpublished cDNA library,
/lone_107 c 110 g 77 t
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                                                                                                                            Score 39; DB 12; Length 359;
Pred. No. 11;
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856 bp DNA linear GSS 17-DEC-2002 msh2_5817.x1 msh Pseudomonas aeruginosa genomic clone msh2_5817, BZ578381
                                                                                                                                                                                                         Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (Dases 1 to 856)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:287"
|Colone="mmb2.5817"
|/clone=lib="mmb2.5817"
|/note="Environmental isolate. Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aeruginosa'
                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Center
University of Washington
Bx 352145, Seattle, WA 98105-2145, USA
Tel: 2062216554
Fax: 2066857244
Email: craymond@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pseudomonas & /mol_type="genomic DNA" /strain="MSH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Cabernet Sauvignon Leaf - CA12EI"
/clone lib="Cabernet Sauvignon Leaf. Sfil; Site_2:
Sfil; CA12EI is a cDNA library of Cabernet Sauvignon
leaves. The leaves were collected on July 25, 2001, in
Napa Valley, California, and represent leaves in
mid-season development. These leaves were verified to be
infected with the bacterial pathogen, Xylella fastidiosa,
based on a diagnostic assay using PCR and Xylella-specific
primer pairs. The plants were asymptomatic at the time of
collection, but later developed symptoms. CDNAs were made
by oligo-dr priming and directionally cloned. 5'and 3'
adaptors were used in cloning as follows:
                                                                                                                    vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids
; Vitaceae; Vitis.
1 (bases 1 to 621)
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                                                                                                                                                                                                                        Goes da Silva, F., Lim, H., Iandolino, A., Baek, J., Jones, K., Walker, M.A. and Cook, D.R.
Transcriptional responses of Vitis vinifera to infection by the bacterial pathogen Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-1' and S'-ATTCTAGAGCCGGCGACAT(10)Nn-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."
CA12E1301IVF_E04 Cabernet Sauvignon Leaf - CA12E1 Vitis vinifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // sex="hermaphrodite"
// dev_stage="Mid-season leaf material"
// lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                                              Contact: Doug Cook
CAES Genome Facility
UC Davis Department of Plant Pathology
1 Shields Ave., Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 661
Email: drcox@ucdavis.edu
Seg primer: GTTATCAGTCGACGGTACC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Vitis vinifera"
/mol type="mkNa"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CA12E13011VF_E04"
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                                                                                                     Vitis vinifera
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1 (Dases 1 to 872)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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pacs1-60_4970.x1 pacs1-60 Pseudomonas aeruginosa genomic clone pacs1-60_4970, genomic survey sequence.
                                                                                                                                                                                                                              0; Gaps
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Score 39; DB 29; Length 856; Pred. No. 14;
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Contact: Chris K. Raymond
Genome Center
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Search completed: December 20, 2003, 06:54:45
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/db_rase="texan:8606"

/dlone="CSODF010YP12"

/tissue type="FETAL BRAIN"

/dev stage="fetal"

/dev stage="fetal"

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Li, W. S. Gruber, C., Jessee, J. and Polayes, D. Pull-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - Fir, Web : www.genoscope.cns.fr
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email: fliangelifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF010DH06QP1.
Location/Qualifiers
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/clone="pacs1-60_4970"
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/clone_lib="pacs1-60"
/note="clinical isolate 1-60 Whole genomic shotgun
library."
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                                                                                                                                                                                                                                                                                                                                                                     /organism="Pseudomonas aeruginosa"
/mol type="genomic DNA"
/strain="1-60"
                         Box 352145, Seattle, WA 98105-2145, USA Tel: 2062216954
Fax: 206687244
Email: craymond@u.washington.edu
Class: shotgun.
Location/Qualifiers
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University of Washington
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                                                                                                                                                                                                                                                                                                                                                                  247 ATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGACATG 306
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                                                                                     67 gragagaccccccraagagagacraacagacccraacacaraacarccagarcragaa 126
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                                                                                                                                                                                 187 GCTTTACTGTCCTGTCTAACCATTCCAGCTTCCGCTTACGAGGTGCGCAACGTGTCCGGG
                                                Gaps
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Best Local Similarity 14.1%; Pred: No. 16; 16; Indels Matches 56; Conservative 174; Mismatches 162; Indels
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MOLECULE TYPE: CI
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                        Sequence:
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                                                                                                                                 Run on:
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ALIGNMENTS

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mat_peptide
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                                                                                                                                                                                                                                 MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                     ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
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GENERAL INFORMATION:
APPLICANT: MAERIENS, GEERT
APPLICANT: BOSNAN, FONS
APPLICANT: BUYER, MARIE-MGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSES: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: 105.A.
ZIP: Z2201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORY disk
MEDIUM TYPE: FLORY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: BLOPPY disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                     61 COGCTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCCTTGGCGCTT
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                                                         ATGCTGGGTAAGGCCATCGATACCCTTACGTGCGGCTTCGCCGACCTCGTGGGGTACATT
                                                                       1 AIGCIGGGIAAGGCCAICGAIACCTIACGIGCGGCTICGCCACCICGIGGGGIACAIT
                                                                                                                  Gaps
                                     ;
0
                 Length 636;
                                      0; Indels
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                100.0%; Score 636; DB 3; L
100.0%; Pred. No. 3.3e-164;
iive 0; Mismatches 0;
                      Query Match
Best Local Similarity 100.
Matches 636; Conservative
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US-08-927-597-13
US-08-612-973-13
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100.0%; Score 636; DB 3; Length 636;
Best Local Similarity 100.0%; Pred. No. 3.3e-164;
Matches 636; Conservative 0; Mismatches 0; Indels C
                #1.25 (EPO)
            OPERATING SYSTEM: PUCLUONING BL.
SOCTUMENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION NUMBER: US 08/612,973
FILING DATE:
APPLICATION NUMBER: US 08/612,973
FILING DATE:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
NAME: BYRNE, THOMAS E.
REFERENCE/DOCKET NUMBER: 32,205
RECISTATION NUMBER: 32,205
RECISTATION NUMBER: 32,005
RECISTANTION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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540

480

360

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300
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Sequence 7, Application US/08927597

Sequence 7, Application US/08927597

Patent No. 6245503

GENERAL INFORMATION:

APPLICANT: BORNAN: CBERT

APPLICANT: BUYSE, MARIE-ANGE

TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

MUMBER OF SEQUENCES: 112

CORRESPONDENCE ADDRESS:

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STREET: USON NORTH GLEBE ROAD

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION NUMBER: US/08/927,597

FILING DATE:

CITASSPERIED: CITATION NUMBER: US/08/927,597
                                      121 CTGGAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTC
                                                                                                                                     181 CTCTTGGCTTTACTGTCCTGTCTGACCATTCCAGCTTCCGCTTATGAGGTGCGCAACGTG
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                                                                                                                                                                                    241 TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNDMERR: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS B.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
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                                          541 CATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCGGCCACATAACGGGTCACCGT
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                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUSSEN, GUS
APPLICANT: BUSSE, MARTYNOFF, GUY
APPLICANT: BUYSE, MARTYNOFF, GUY
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PRRIEIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROFINIS FOR DIAGNOSTIC AND THERAPEUTIC USE
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYEER EADABLE FORM:
MEDIUM TYEER EADABLE FORM:
MEDIUM TYEER EADABLE FORM:
MEDIUM TYEER EADABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
TYEER APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
TYEING DATE: 11-MAR-1996
                                                                                                               601 ATGGCTTGGGATATGATGATGAACTGGTACTAATAG 636
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                                                                                     601 ATGGCTTGGGATATGATGATGAACTGGTACTAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
RECISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                   RESULT 3
US-08-612-973-7
Sequence 7, Application US/08612973
; Patent No. 6150134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY:
LOCATION:
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; LOCATION:
US-08-612-973-7
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APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 ONTH GLEBE ROAD
                                                                                                                                                                      ZID: 2201-4714

ZIP: 2201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: IMP PC LOSS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 10/08/612,973
FILING DATE: 11-MAR-1996
JELING DATE: 11-MAR-1996
JELING DATE: 11-MAR-1996
JELSSIPPROTION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELEPHONE: (702) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
INFORMATION POR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
JTYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.6
Matches 613; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                         CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGI.
MOLECULE TYPE: CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NC
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                          Length 633;
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                                                                                                                                                                                                                                                                         Score 612.8; DB 3;
Pred. No. 7e-158;
0; Mismatches 12;
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TELEFAX: (703) 816-4100
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                               96.4%;
98.1%;
                                                                                                                                                                                                                                                                               Query Match 96.4 Best Local Similarity 98.1 Matches 620; Conservative
                                                                                                                                                                                                                     NAME/KEY: mat peptide;
LOCATION: 1..627
US-08-927-597-7
                                                                                                                         MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                             1..630
                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                               LOCATION:
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                                                                                  1 ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT
                              Gaps
                                ;
Length 795;
95.0%; Score 604; DB 3; Length 79
97.6%; Pred. No. 1.9e-155;
tive 0; Mismatches 15; Indels
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RESULT 5
US-08-612-973-5
; Sequence 5, Application US/08612973
; Patent No. 6150134
; GENERAL INFORMATION:

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Gaps

120 120 180 180 240 240

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300 360 420 420 480

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241 TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG 300
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APPLICANT: MORNAN, FONS
APPLICANT: BORNAN, FONS
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDEHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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0
                                                                                                                                                              Length 795,
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                               15;
                                                                                                                                                           Score 604; DB 3; 1
Pred. No. 1.9e-155;
0; Mismatches 15;
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; Patent No. 6150134
                                                                                                                                                           Query Match
Best Local Similarity 97.6%;
Matches 613; Conservative 0
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STATE: VIRGINIA
COUNTRY: U.S.A.
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      ; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-927-597-5
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APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARIYINOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROFFIED HEPATITIS C VIRUS ENVELOPE

TITLE OF INVENTION: PROFFIED HEPATITIS C VIRUS ENVELOPE

TITLE OF INVENTION: PROFFIED HEPATITIS C VIRUS ENVELOPE

TITLE OF INVENTION: PROFFIED HEPATITIS C VIRUS ENVELOPE

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ZIP: 22201-4714
COMPUTER READABLE LOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/927,597
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APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08927597
Patent No. 6245503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (703) 816-4000
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 795 base pairs
nucleic acid
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ADDRESSEE: NIXON & V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
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US-08-927-597-5
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Sequence 47, Application US/08927597

Patent No. 6245503

GENERAL INFORMATION:
APPLICANT: BOSMAN, FONS
APPLICANT: BUXBS, MARIE-MARE
APPLICANT: BUXBS, MARIE-MARE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSES INORTH GLEBE ROAD
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: RINGTON
CONTRADON TO THE TREET OF THE TRE
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CONTRY.

ZIP: 22201-4714

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
RAPPLICATION NUMBER: US/08/927,597
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CLASSTRICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE:
Il-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2082 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                   605 CTTGGGATATGATGATGACTGGT 628
                                                                                                                                                               605 CTTGGGATATGATGACTGGT
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Best Local Similarity 97.8
Matches 610; Conservative
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LOCATION:
FEATURE:
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US-08-927-597-47
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                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: PATENTIN DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYREW, THOWAS E.
REGISTRATION NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2082 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TYPE: CDM.
TYPOLIGITICAL: NO
HYPOTHETICAL: NO
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97.8%; Pred. No. 1.1e-154;
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Best Local Similarity 97.8
Matches 610; Conservative
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; LOCATION: 1..2076
US-08-612-973-47
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ANTI-SENSE: NO
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545 AGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     896 AGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 AGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTTTTCTTCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 TGGGTAAGGCCATCGATACCCTTACGTGCGGCTTCGCCGACCTCGTGGGGTACATTCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         94.6%; Score 601.6; DB 3; 97.8%; Pred. No. 1.2e-154; ive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             956 CTTGGGATATGATGATGAACTGGT 979
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US-08-927-597-49
; Sequence 49, Application US/08927597
; Patent No. 6245503
; GENERAL INFORMATION:
TELEPAN: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2433 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 97.8
Matches 610; Conservative
                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                   MOLECULE TYPE: CDNA HYPOTHETICAL: NO PEATURE:
                                                                                                                                                                                                                                                                                                       1..2430
                                                                                                                                                                                                                                                                                               LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
; LOCATION:
US-08-612-973-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 '
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                                                                                                                                                             244
                                                                                                                                                                                                                                                  GGATGTACCATGTCACGACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGACA 304
                                                                                                                                                                                                                                                                                                                                               364
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGTAGCGCTCACCCCACGCTCGCGGCTAGGAACGCCAGCATCCCCCACTACAACAATAC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTAGCGCTCACCCCCACGCTGCAGCTAGGAACGCCAGCGTCCCCACCACGACATAC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        545 AGACGGTGCAGGACTGCAATTGCTCAATCTATCCGGCCACATAACGGGTCACCGTATGG 604
                                                                                               125 AGGACGCGCGTGAACTATGCGAAATTTGCCCGGTTGCTCTTTCTCTATCTTCTCTTCCTCT
                                                                                                                                                                                    185 TGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTCCCG
                                                                                                                                                                                                                                                                                                                                                                       305 TGATCATGCACACCCCCGGGTGCGTGCCTTCGGGTTCGGGAACAACTCTTCCCGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 GAGGCCACGTCGATTTGCTCGTTGGGGGGGGCTGCTTTCTGTTCCGCTATGTACGTGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 ACCTCTGCGGATCTGCTTCCTCGTCTCCCCAGCTGTTCACCATCTCGCCCTCGCCGGCATG
                                                                                                                                                          185 TGGCTTTACTGTCCTGTCTAACCATTCCAGCTTCCGCTTACGAGGTGCGCAACGTGTCCG
                                                                                                                                                                                                                                                                                                                                             TGATCATGCACACCCCGGGTGCGTGCCTTGCGTTCGGGAGACAACTCTTCCCGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGCCACGTCGATTTGCTCGTTGGGGCGCCTCTTTCTGTTCCGCTATGTACGTGGGGG
                                                                    AAGACGCCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GU
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROPEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

ZIF: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,973

FILING DATE: 11-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTGGGATATGATGATGAACTGGT 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGGGATATGATGAACTGGT 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1487-10
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Patent No. 6150134
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INPORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 148
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON
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424

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APPLICANT: Okamoto, Hiroaki
APPLICANT: Nakamura, Tetsuo
TITLE OF INVENTION: DULGONUCLEOTIDE PRIMERS, AND THEIR
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B
TITLE OF INVENTION: HEPATITIS VIRUS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young,
ADDRESSEE: L.L.P.
STREET: 1850 M Street, N.W., Suite 800
CITY, Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         896 AGACGGIGCAGGACICCAATIGCICAATCIATCCCGGCCACATAACGGGICACCGIAIGG 955
                                                                                                                                                                      485 Arcrenererererererererecedengererecarererereregenes
                                                                                                                                                                                                                                                                                                                                                                                                                545 AGACGGTGCAGGACTGCAATTGCTCAATCTATCCGGCCACATAACGGGTCACCGTATGG
                                                                                                                                                                                                                                                                                     GGGTAGGGCTCACCCCACGCTCGCGGCTAGGAACGCCAGCATCCCCACTACAACAATAC
                                                                                                                                                                                                                                                       425 GACGCCACGTCCATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGGG
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTINE PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/470,426B
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US/08/470,426B
PRICK APPLICATION NUMBER: US/08/470,426B
FILING APPLICATION NUMBER: US/08/470,426B
ATTONNUMBER: US-JUN-1990
ATTONNEY/AGBNT INPORMATION:
ATTONNEY/AGBNT INPORMATION:
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NAME: Weilacher, Robert G.
REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06/59-47083.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2811
TELEFAX: (202) 659-1462
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        605 CTTGGGATATGATGATGAACTGGT 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08470426B Patent No. 5856458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1539 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124
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APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROFIEID HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROFIEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: 112
CORRESPONDENCES: 113
CORRESPONDENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22201-47/4

ZIP: Z2201-47/4

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: STATE C COMPATIBLE
OPERATION STATE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE: THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION INFORMATION:
TELEPHONE: (703) 816-400
TELECHONE: (703) 816-400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-400
TELECOMMUNICATION INFORMATION:
TELEPHONES: SEQUENCE CHARACTERISTICS:
LENGTH: 2433 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGLE
AND STRANDEDNESS: SINGLE
AND STRANDEDNESS: SINGLE
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94.6%; Score 601.6; DB 3;
Best Local Similarity 97.8%; Pred. No. 1.2e-154;
Matches 610; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                              1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , NAME/KEY: mat_peptide
, LOCATION: 1..2427
US-08-927-597-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..2430
                                                                                                                                                                                                                                                                                                                               CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
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1040 GGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAATGCCAGGGTCCCCACTACGACAATAC 1099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .125 AAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          740 TCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCTTGGCACACGGTGTCCGGGTTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 TGGCTTTACTGTCCTGTCTAACCATTCCAGCTTACGAGGTGCGCAACGTGTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.0%; Score 553.6; DB 2; 92.9%; Pred. No. 1.3e-141; iive 0; Mismatches 44;
                       PERENTIAL ACTUAL NUMBER: US/08/470,426B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PURSA APPLICATION DATA:
APPLICATION NUMBER: JP 2-153402
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weilacher, Robert G.
REGISTRATION NUMBER: 20,531
REFERBINCE/DOCKET NUMBER: 06/59-47083.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2811
TELEPHONE: (202) 659-1462
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1863 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.9
Matches 580; Conservative
             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-470-426B-14
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Sequence 14, Application US/08470426B
Patent No. 5856458
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Okamoto, Hiroaki
APPLICANT: Okamoto, Hiroaki
APPLICANT: Okamoto, Hiroaki
APPLICANT: NAMMER.
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-B
TITLE OF INVENTION: HEPATITIS VIRUS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: L.L.P.
STREET: 1850 M Street, N.W., Suite 800
CITY: Washington
                                                                                                                                     356 IGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGATCTCATGGGGTATATTCCCC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   896 AGACAGTGCAGGACTGCTAAATCTATCCGGGCCATTTATCAGGTCACGGATGG 955
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                                                         Gaps
                                                                                                        TGGGTAAGGCCATCGATACCCTTACGTGCGGCTTCGCCGACCTCGTGGGGTACATT
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          Length 1539;
                                                         Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
     Score 553.6; DB 2;
Pred. No. 1.2e-141;
0; Mismatches 44;
                                                      0; Mismatches
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92.9%;
Query Match
Best Local Similarity 92.9
Matches 580; Conservative
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US-08-470-426B-14
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739 124 799 184 859 244

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1039

979 364 424

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544

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TGGCTTTACTGTCCTGTCTAACCATTCCACCTTACGAGGTGCGCAACGTGTCCG 244
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490 ATCTCTGTGGATCTGCTTCCTCGTTTCCCAGCTGTTCACTTTCTCACCTCGTCGGCATG
                                                                                                                                                                                                                                 550 AGACAGTACAGGACTGCTACTCTATCTATCCCGGCCACTTGACAGGTCATCGCATGG
                                                                                                                             545 AGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TOYOSHIMA, and Michinori KOHARA
APPLICANT: TOYOSHIMA, and Michinori KOHARA
TITLE OF INVENTION: NON-A NON-B HEPATITIS-SPECIFIC
TITLE OF INVENTION: ANTIGEN AND ITS USE IN HEPATITIS
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: 130 Water Street
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Best Local Similarity 92.6%; Pred. No. 7.9e-141;
Matches 578; Conservative 0; Mismatches 46;
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ZIP: 02109-4280

COMPUTER READABLE FORM:
MEDIUM TYPE: Disfectre
COMPUTER: IBM COMPAIDLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSCN VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,093A
FILING DATE: MAY 24, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/081,072
FILING DATE: JUNE 22, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/726,141
FILING DATE: UNP 8, 1991
CLASSIFICATION DATA:
FILING DATE: UNP 8, 1991
CLASSIFICATION POR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 932 base pairs
TYPE: nucleic acid
STARADEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                             628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633
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US-08-449-093A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-449-093A-15
Sequence 15, Application US/08449093A
Patent No. 5662906
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       605 CTTGGGATATGATGATGAACTGGT
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STATE: Ma
COUNTRY:
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                                                                                                    US-08-081-072-15;
Sequence 15, Application US/08081072;
Sequence 15, Application US/08081072;
Patent No. 5641654
GENERAL INFORMATION:
APPLICANT: No. 5641654oru MAKI, Kenjiro YAMAGUCHI, Ayumi, APPLICANT: TOYOSHIMA, and Michinori KOHARA
APPLICANT: TOYOSHIMA, and Michinori KOHARA
TITLE OF INVENTION: NON-A NON-B HEPATITIS-SPECIFIC
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Dike, Bronstein, Roberts & Cushman
STREET: DISO Water Street
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US-08-081-072-15
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: December 20, 2003, 07:03:03 Job time: 47.8681 secs
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ORIGINAL SOURCE:
ORGANISM: Hepatitis C virus
IMMEDIATE SOURCE:
CLONE: pUCO10
                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELESX: 24885.OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Best Local Similarity 92.5
Matches 577; Conservative
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LOCATION:
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APPLICANT: MIYAMURA, TATSUO
APPLICANT: SAITO, IZUMU
APPLICANT: SAITO, IZUMU
APPLICANT: HONDA, YOSHIHARU
APPLICANT: HONDA, YOSHIKAZU
APPLICANT: SEKI, MAKOTO
TITLE OF INVENTION: METHOD FOR PRODUCING ECTOPROTEIN
TITLE OF INVENTION: HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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STREET: 1755 S. Jefferson Davis Highway, Suite 400
STATE: Virginia
COUNTRY: U.S.A.
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CIP: 2202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRET PAPLICATION DATA:
APPLICATION NUMBER: US/08/462,195
FLING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/446,303
FLING APPLICATION NUMBER: US/08/446,303
FLING DATE: 11-JUN-1993
APPLICATION NUMBER: US/08/74,584
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: US/08/074,584
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: 22-M2-1995
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5789544man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
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Patent No. 5789544
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Maximum Match 1008
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | A48683 Sequence 21 AR15736 Sequence AX68502 Sequence AX68502 Sequence AX68502 Sequence AX68505 Sequence AX68506 Sequence AX68506 Sequence AX68506 Sequence AX68506 Sequence AX68508 Sequence AX68509 Sequence AX68508 Hepatitis AF16505 Hepatitis AX03625 Sequence | ONA linear PAT 07-MAR-1997 Buyse, M. PROTEINS FOR DIAGNOSTIC AND |
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Other publication CA 2172273 960215 Other publication AU 3382495 960304. Location/Qualifiers
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Maertens, G., Bosman, F. and Buyse, M.A.
Purified Hepatitis C Virus envelope proteins
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Viruses; ssRNA positive-strand viruses,
Hepacivirus.
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Parent: WO 07055548-A 21 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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Viruses; ssRNA positive-strand viruses,
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Other publication CA 2172273 960215
Other publication AU 3382495 960304.
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| Db 601 ATGGCTTGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTG 660 Qy 589 CTCCGGATCCCAAGCTGTGTGTGTGGTGGGGGGGCCCATTGGGGGGGTCCTGGCG 648 | Db 781 TTGCTCCCTAATAG 795 RESULT 7 AX452754 LOCUS DEFINITION SEQUENCE 5 from Patent EP1211315. ACCESSION AX452754 VERSION AX452754 GI:21712439 KEYWORDS SOURCE Hepatitis C virus ORGANISM Hepatitis C virus Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae; | REFERENCE 1 AUTHORS Maertens, G., Bosman, F., de Martynoff, G. and Buyse, M.A. TITLE Recombinant vectors for producing how envelope proteins JOURNAL Patent: BP 12113155 A 5 05-JUN-2002; Innogenetics N.V. (BE) BEATURES Location/Qualifiers Source //ordanism="Henalitis C virus" | /mol_type="genomic DNA" /db_xref="taxon:11103" 1. 792 /note="unnamed protein product" /codon start=1 /protein id="CAD38067.1" /db_xref="G1:21712440" /translation="MiGKVIDM:TGGRADH.WGADH.AGGAARALAHGWRULEDG | VNYATGNLPGCSFSIFLALLSCLTVPASAYEVRNVSGMYHVTNDCSNSSIVYEAADM IMITPGCVPCVRSNNSSRCWVALTFTLAARNASVPTTTIRRHVDLLVGAAAFCSAMYV GDLCGSVFLVSQLFTISPRHETVQDCNCSIYPGHITGHRMAWDMMMNNSPTTALVVS QLIRIPQAVVDMVAGAHWGVLAGLAYSMVGNWAKVLIVMLLFAP" 1 . 789 | Query Match 88.7%; Score 641; DB 6; Length 795; Best Local Similarity 90.9%; Pred. No. 6.3e-130; Matches 723; Conservative 0; Mismatches 0; Indels 72; Gaps 1; | QY 1 AIGTIGGGTAAGGTCATCGATACCTTACATGGGGCTTCGCCGACCTCGTGGGGTACATT 60 | Qy 61 CCGCTCGTCGGCGCCCCCTAGGGGCGCTGCCAGGGCCTTGGCGATGGCGTCCGGGTT 120 | QY 121 CTGGAGGAGGGGGGGAACTATGCCCGGTTGCTCTTTCTCTATCTTC 180 | QY 181 CTCTTGGCTTTGCTGTCTGTCTGACCGTTCCGGCTTATGAAGTGCGCAACGTG 240 | |
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| Qy 709 TTTGCTCCCTAATAG 723 Db 781 TTTGCTCCCTAATAG 795 AR157325 795 bp DNA linear PAT 17-OCT-2001 DEFINITION Sequence 5 from patent US 6245503. ACCRSSION AR157325 ACCRSSION AR157325 | | Covery Match Query Match Best Local Similarity 90.9%; Pred. No. 6.38-130; Matches 723; Conservative 0; Mismatches 0; Indels 72; Gaps 1; A TGTTGGGTAAGGTCATGGATACCTTACATGGGGCTTGCCGACGTGGGGTACATT 60 | | | 301 GACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGC 360 | 361 TGCTGGGTGGCTCACCCCACGCTCGCAGGTAGGAACGCCAGCGTCCCCACCACGAGA 420 | 421 ATACGACGCACGTCGAT 438 | 439 | 469 CATGAGACGGTGCAGGACTGCAATTGGTCAATCTATCCCGGCCACATAACGGGTCACCGT 528 | |

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                                      Maertens, G., Bosman, F. and Buyse, M.A.
Purified Hepatitis C Virus envelope proteins for diagnostic itherapeutic use
Patent: WO 02055548-A 5 18-JUL-2002;
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/mol type="genomic DNA"
/db_xref="taxon:11103"
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
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Patent: US 6245503-A 47 12-JUN-2001;
Location/Qualifiers
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S Maertens, G., Bosman, F., De, M.G. and Buyse, M.

PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND
THERAPEUTIC USE

L PATENT: WO 9604385-A 47 15-FEB-1996;

INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.

L. 2082

/organism="unidentified"
/mol_type="genomic DNA"
/db zref="taxon:32644"

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                                                               CGACGCCACGTCGAT---------
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/db_xref="taxon:11103"
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47 from Patent EP1211315.
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VGDLCGSVFLVSQLFTISPRRHETVQDCNCSIYPGHITGHRMAMDMMMNMSPTTALVV
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GCPERLASCRSIDKFAQGWGPLTYTEPNSSDQRPYCWHYAPRPCGIVPASQVCGPVYC
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PPCNIGGAGNNTLTCPTDCFRKHPEATYARCGSGPWLTPRCMVHYPYRLMHYPCTVNF
TIFKVRMYVGGVEHRFEAACNWTRGERCDLEDRDRSELSPLLLSTTEWQILPCSFTTL
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   424 CGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG 483
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Maertens, G., Bosman, F., De, M.G. and Buyse, M.
PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND
                                                                                                                                544 GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG
                                                           GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG
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Patent: WO 9604385-A 49 15-FEB-1996;
INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.
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WO9604385.
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GLOCGSVPTWOGLTISPRRHETVQDCNCSTYPGHTTGHRMAMDMAMWSPTTALVVS
GLLR PQAVVDWVAGAHWGVLAGLAYYSWVGWAKVLVVMLLPAGVDGHTRVSGGAAA
SDTRGLYSLFSPGSAQKIQLVMTNGSWHINTTALNCNDSLQTGFPAALFYKHKNSGG
CPERLASCRSIDKFAQGWGPLTYTEPNSSDQRPYCWHYAPRPGGIVPASQVCGPVYCF
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PCN I GGAGNNTL TCPTDCPRKHPEATYARCGSGPWLTPRCMVHY PYRLWHY PCTVNFT
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                                                       no DNA stage; Flaviviridae;
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Purified Hepatitis C Virus envelope proteins for diagnostic and
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Pred. No. 2.1e-126;
0; Mismatches 2;
                 Hepatitis C virus
Hepatitis C virus
Viruses; seRNA positive-strand viruses,
Hepacivirus.
                                                                                                                                                                                                                                                                                                             'note="unnamed protein product"
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                                                                                                                                            therapeutic use
Patent: WO 02055548-A 47 18-JUL-2002;
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Location/Qualifiers
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/product="unnamed"
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Best Local Similarity 90.5%;
Matches 708; Conservative
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Maertens,G., Bosman,F., De Martynoff,G. and Buyse,M.-A.
Purified hepatitis C virus envelope proteins for diagnostic
therapeutic use
Patent: US 6245503-A 49 12-JUN-2001;
Location/Qualifiers
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MINHTPGCVPCVRENNSSCROWALTPTLAANASAPTTTIRHVDLIVGAAAFCSAMY
VGDLGGSVFLVSQLFTISPRHETVQDCNCSIYPGHITGHRMAMDMANWSPTTALVV
SQLLRIPPQAVVNYAGAHWGVLAGLAYYSWCUNAFVLVWILLEAGVOGHTYNSGGAA
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LLLALPPRAYA"
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                                     775 CGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG 834
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364 TGGGTAGGGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACCACGACAATA
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Hepatitis C virus

ABK91429 ABK91430

ABK91428

ABK91432

Sequence:

Title:

. :

Run

Searched:

Database

ABK91424 ABK91425

Partial HCV non-st Hepatitis C virus DNA encoding HCV p Hepatitis C virus Hepatitis C virus Hepatitis C virus Fragment #5 isolat

AAQ81559 AAQ80498

AAQ64068

AAT30386

Plasmid pIDKE2 DNA Cuticle protein 1 NANB hepatitis vir NANBHV genomic fra

ABA03491 AAQ43889

AAQ63753

Fragment #6 isolat HCV-S1 full-length

ALIGNMENTS

AAD33038

HCV gene 1. Hepat Hepatitis C genome Non-A, non-B hepat S'UTR/CORE/ENV/NS1

ABK91433 AAD25332 ABK91427 AAD25331 AAA98965 AAT12962 AAL48926 AAC66981

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9413
9413
1562
1953
2187
2540
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2580
9609
                                    VPI; 1996-129401/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus.
29-JUL-1994;
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AAT12961;
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 RESULT
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                                                                                                                                                      ATGTTGGGTAAGGTCATCGA.....TACTCTTTGCTCCCTAATAG 723
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          version 5.1.6
- 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                         nucleic search, using sw model
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AAL48914
AAL48939
AAT12973
AAT12974
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AAL48925
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Gapop 10.0 , Gapext 1.0
              GenCore (c) 1993
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Maximum DB seq length: 200000000
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Match Length DB
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HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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AAT12961 standard; DNA; 723
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                                                                                                                 24-SEP-1996 (first entry)
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Result

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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. Cr in vectors for the production of recombinant E1, E2, and E1/E2 proteins. Cc invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a crew constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated conformation of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are mercive with human sera than those isolated by known
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proteins - in presence of di:sulphide bond cleavage agent, to
produce proteins suitable for direct use in vaccines or diagnostic
assays of HCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 723 BP; 126 A; 220 C; 208 G; 169 T; 0 other;
                                                                                  21; 146pp; English
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Best Local Similarity 100.0%;
warrhes 723; Conservative 0
                                                                                         Claim 23; Fig
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV El and/or E2 proteins are useful as against HCV. The recombinant HCV screening and confirmatory antibody vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for radising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT 120
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CAAGCTGTCGTCGACATCGTGGCGGGCCCCATTGGGGAGTCCTGGCGGGTCTCGCCTAC 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
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                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; El protein; E2 protein; infection; gene; virucide; immunostimulant; vaccine; ds.
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                                                                                                                                                                                                                                                                                                               Hepatitis C virus clone HCCI37 El protein coding sequence.
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                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                     AAL48925 standard; DNA; 723
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30-AUG-2001; 2001US-315768P.
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3; Conservative
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Matches 723;
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                         CTGGAGGACGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTC
                                        CTGGAGGACGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTC
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HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
              AAT12705 standard; DNA; 795
                                             (first entry)
                                                            HCV El construct HCCI10A.
                                                                                                            Hepatitis C virus.
                                                                                                                           WO9604385-A2
                                             23-SEP-1996
                             AAT12705
     RESULT 3
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94EP-0870132 95WO-EP03031

31-JUL-1995; 29-JUL-1994; (INNO-) INNOGENETICS NV.

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361 IGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCCAGCGTCCCCACCACGACA

480 468 540

ATACGACGCCACGTCGATTTGCTTGGGGGGGGCTGCTTTCTGTTCCGCTATGTACGTG

ATACGACGCCACGTCGAT----

421 421

g ò 셤 8 481 GGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGG

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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1
and E2 protein coding sequence constructs. These sequences are included
in vectors for the production of recombinant E1, E2, and E1/E2 proteins.
The recombinant proteins can then be isolated using a method of the
invention. In the method, the envelope proteins are purified by
carrying out a disulphide bond cleavage, or a reduction step with a
disulphide bond cleavage agent, after 1981s of recombinant host cells.
The constructs containing the purified HCV envelope proteins can be used
for vaccinating humans against HCV, for in vitro detection of HCV
contributes containing the purified HCV envelope proteins can be used
for vaccinating humans against HCV, for in vitro detecting one or
more serological types of HCV present in a biological sample. The
constructs can also be immobilised on a solid substrate and incorporated
into a reversed phase hybridisation assay for determining the presence or
the genotype of HCV. The new purification method preserves the
conformation of the recombinantly expressed E1, E2 and E1/E2, and
eliminates contaminating proteins. Antigens isolated using this method
are more reactive with human sera than those isolated by known
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                                                                                   Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins sultable for direct use in vaccines or diagnostic assays of HCV
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Pred. No. 3.2e-163;
0; Mismatches 0; Indels 7;
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                      Maertens
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Best Local Similarity 90.9%;
Matches 723; Conservative
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Length 795;

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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligometric recombinant envelope proteins selected from an E1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for the view monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence in the exemplification of the invention.
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                                                                    CTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGCG
CATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGT
             ATGGCTTGGGATATGATGATGACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus clone HCCI10A B1 protein coding sequence.
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30-AUG-2001; 2001US-315768P.
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P-PSDB; AA018661.
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Sequence 795 BP; 130 A; 240 C; 231 G; 194 T; 0 other;

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                                                                                                                              TCCGGGATGTACCATGTCACGAACGACTGCTCCAAGCATTGTGTATGAGGCAGCG
                                                                                                                                                                              GACATGATCATGCACACACCCCGGGTGCGTGCCCTGCGTTCGGGAAGAACAACTCTTCCCGGC
                                        1 ATGITGGGTAAGGTCATCGATACCTTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT
                                                                  ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT
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             Gaps
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             72;
              Indels
Score 641; DB 24;
Pred. No. 3.2e-163;
                                                                                                                                                                                                                                             421 ATACGACGCCACGTCGAT------------
               0; Mismatches
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 88.7%;
90.9%;
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Best Local Similarity 90.9
Matches 723; Conservative
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                                                                                                                                                                                                                                                                 GCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
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                                                                                                                                                                                 GAGACGGTGCAGGACTGCAATTGČTCAATCTATCCCGGCCACATAACGGGTCACCGTATG
                                                                                                                                                                                                        544 GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG
                                                                                                                            604 GCTTGGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
                                                           424 CGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunishing humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody rests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGTCGCCCCCCCTAGGGGCGCCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to new therapeutic vaccine compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention
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                                                                                                                                                                                                                                                                                                                                                                                                      New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
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Pred. No. 1e-158;
0; Mismatches 2; Indels 72;
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virucide; immunostimulant; vaccine;
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ilarity 90.5%;
Conservative
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                                                                                                                                                                                                                                                             (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                       Bosman F,
                                                                                                                                                                                                                                                                                                                                           WPI; 2002-599657/64
P-PSDB; AA018678.
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ses 708; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified RCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyphing assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed El, E2 and El/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known
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                                                                                                                                                                                               Score 624.8; DB 17; Length 2086;
Pred. No. 1e-158;
0; Mismatches 2; Indels 72;
                                                                                                                                                                        Sequence 2086 BP; 366 A; 635 C; 601 G; 484 T; 0 other;
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Best Local Similarity 90.5%;
Matches 708; Conservative C
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AATI2704-T12709 and AATI2961-T12974 represent hepatitis C virus (HCV) El cand E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. In vectoria for the production of recombinant E1, E2, and E1/E2 proteins. Cr the recombinant proteins can then be isolated using a method of the carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a servicyping assay for detecting one or antibodies in a sample, and in a servicyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated conto a fHCV present in a say for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and conformation of the recombinantly expressed E1, E2 and E1/E2, and conformation expressed than those isolated by known are meaning proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   purifying recombinant hepatitis C virus (HCV) E1 and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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Pred. No. 1.1e-158;
0; Mismatches 2; Indels 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 2433 BP; 434 A; 745 C; 714 G; 540 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 23; Fig 21; 146pp; English.
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ilarity 90.5%;
Conservative 0
                                                                              DNA; 2433
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                                                                                                                                                                             HCV El construct HCCI66.
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les 708; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-129401/13.
                                                                              AAT12974 standard;
                                                                                                                                                                                                                                                                                 Hepatitis C virus.
785
                                                                                                                                                                                                                                                                                                                 WO9604385-A2
                                                                                                                                                                                                                                                                                                                                                                                31-JUL-1995;
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific Oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or B2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                   is a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 CTCGTCGCCCCCCCTAGGGGGCGCTGCCAGGCCCCTGGCGCATGGCGTCCGGGTTCTG
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                                                                                                             one purified
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                                                                                                           New therapeutic vaccine compositions comprising at least one purifit recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 613.8; DB 24; Length 2434;
Pred. No. 1e-155;
0; Mismatches 2; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                         Example 2; Page 212-215; 243pp; English
                                 Buyse M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 708; Conservative
   (INNO-) INNOGENETICS NV
                                 Bosman F,
                                                              WPI; 2002-599657/64.
P-PSDB; AAO18679.
                                                                                                                                                              from HCV infection
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                                 Maertens G,
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Best Local S:
Matches 708,
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                                                                                                                                                                                                                                                      TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACAATA 423
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                                                                                                                                            GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
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                  GAGGACGGCGTGAACTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTTATCTTCTCTC
                                                                                                                          GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E2 protein; infection; ds.
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virucide; immunostimulant;
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Sequence 606 BP; 109 A; 193 C; 167 G; 137 T; 0 other;
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                             82.7%;
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                               Query Match
Best Local Similarity 99.5
Matches 600; Conservative
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                                                                                                           1074
                                   1014
                                                            650
             590
                                                                                                                                                                                                                                                                                                                                                 HCV, E1; E2; disulphide bond cleavage, envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
           GGCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCT
                         CCGGATCCCACAAGCTGTGGTGGACATGGTGGCGGGGCCCCATTGGGGAGTCCTGGCGGG
                                                                           Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maertens G;
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541 AȚGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCȚCCGGATCCCA 600
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                                                                                       Gaps
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virucide; immunostimulant; vaccine; ds.
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Score 598.2; DB 17; Length 606; Pred. No. 1.1e-151; Mismatches 3; Indels 0;
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541 ATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCTC 600

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                                                                                                                                                                   New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
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Pred. No. 1.1e-151;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 606 BP; 109 A; 193 C; 167 G; 137 T; 0 other;
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30-AUG-2001; 2001US-315768P
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nes 600; Conservative
                                     (INNO-) INNOGENETICS NV
                                                                           Maertens G, Bosman F,
                                                                                                              2002-599657/64.
                                                                                                                                                                                                                             from HCV infection
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1
and E2 protein coding sequence constructs. These sequences are included
to vectors for the production of recombinant E1, E2, and E1/E2 proteins.
The recombinant proteins can then be isolated using a method of the
trention. In the method, the envelope proteins are purified by
c arrying out a disulphide bond cleavage, or a reduction step with a
disulphide bond cleavage agent, after lysis of recombinant host cells.
The constructs containing the purified HV envelope proteins can be used
for vaccinating humans against HCV, for in vitro detection of HCV
artibodies in a sample, and in a serotyping assay for detecting one or
more serological types of HCV present in a biological sample. The
constructs can also be immobilised on a solid substrate and incorporated
tito a reversed phase hybridisation assay for determining the presence or
the genotype of HCV. The new purification method preserves the
conformation of the recombinantly expressed E1, E2 and E1/E2, and
eliminates contaminating proteins. Antigens isolated using this method
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                                                                                                                                                                                                                                                                   HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eliminates contaminating proteins. Antigens isolated using that emore reactive with human sera than those isolated by known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.6%; Score 597; DB 17; Length 636; 100.0%; Pred. No. 2.3e-151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Fig 21; 146pp; English.
                                                                                                                        H.
                                                                                                                        AAT12964 standard; DNA; 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-EP03031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94EP-0870132
                                                                                                                                                                                           24-SEP-1996 (first entry)
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es 597; Conservative
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                                                                                                                                                                                                                                  construct HCCI40
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                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
 601 CAA 603
                                   601 TAA 603
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                                                                                                                                                           AAT12964;
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421 ATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTG 480
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                  The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and specific oligomeric recombinant envelope proteins selected from an El and specific oligomeric recombinant envelope proteins selected from an El and useful for inducing HCV specific antibodies or for immunising humans against HCV. The recombinant HCV El and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for the vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                   Score 597; DB 24; I
Pred. No. 2.3e-151;
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 597; Conservative 0; Mismatches
Page 179-180; 243pp; English.
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                                                                                                    CTCTTGGCTTTGCTGTCTGACGGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG
                            Hepatitis C virus; HCV; El protein; El protein; infection; gene; virucide; immunostimulant; vaccine; ds.
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30-AUG-2001; 2001US-315768P.
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hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
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/note= "The polyprotein consists of the Core, El,
foce= "The polyprotein consists of the Core, El,
F2. P7, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins"
replace (3625,G)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS5, or EMCV IRES mutations, respectively. The location of the NS3, CNS5, or EMCV IRES mutations, respectively. The location of the expression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell; (4) producing an HCV (hepatitis C virus) replicon enhanced cells made in the continuity. The HCV replicon, (5) an HCV replicon enhanced cells made in the continity HCV replicons and HCV replicon enhanced cells are useful in cutivity. The HCV replicons and HCV replicon enhanced cells are useful in cutivity. The HCV replicon and expression, and HCV and host cell continuing the ability of a compound to modulate one or more HCV continues of the measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as sliver failure, cirthosis and hepatocellular carcinoma. The present sequence is the HCV replicon Con 1, used as a basis for the adaptive mutations of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication and expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCGTCGGCCCCCCTAGGGGGCGCTGCCAGGCCCTGGCGCATGGCGTCCGGGTTCTG
                                                                                                                                                                                                /product= "HCV polyprotein"
/note= "The polyprotein consists of the Core, E1,
E2, P7, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins"
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hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV; internal ribosome entry site; IRES; NS5A; HCV replication.
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                                                                                                                             Location/Qualifiers
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                                                                        Hepatitis C virus.
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P-PSDB; ABG32451.
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/note= "The polyprotein consists of the Core, El,

E2, P7, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) NS3 or HCV NS5 encoding respectively. The location of the internal ribosome entry site (IRES) region coding for one or more NS3, contactions are detailed in the specification. Also included are mutations are detailed in the specification. Also included are cutations are detailed in the specification. Also included are mutations are detailed in the specification. Also included are comparable acids, which is transcriptionally coupled to an the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell cacids; (3) a recombinant cell produced by introducing the altered nucleic acids; (4) producing an expectation and hepatican acids; (3) an HCV replicon enhanced cells made in the continual HCV replicons and HCV replicon enhanced cells are useful in extractions, producing the ability of a compound to affect HCV cuteractions, producing HCV RNA and proteins, and providing as system interactions, producing HCV RNA and proteins, and providing as system continuities e.g. to discover drugs which may treat HCV mediated activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV replicon Con 1 mutant of the invention. Was created by the indexer using the HCV sequence appearing as
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                                                                                                                                                                                                                                                                                                                                   New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGGCTITICCIGICCIGICTICACCGTICCACTICCGCTIAIGAAGTGCGCAACGIGTCC
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                                                                                              16-JAN-2002; 2002WO-EP00526.
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New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication and expression -

Claim 9; Page -; 69pp; English.

The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomycoardities virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression vector comprising a nucleocide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing the altered nucleic acids; (4) producing an exogenous promoter; (2) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an every (hcy replicon enhanced cells made in the contributy. The HCV replicon enhanced cells are useful in structional HCV replicons and HCV replicon enhanced cells are useful in cativity. The HCV replicons and HCV replicon enhanced cells are useful in the studying HCV replication and expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system continues are producing HCV RNA and proteins, and providing a system continues such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV replicon con 1 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV sequence appearing as

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Sequence 9605 BP; 1909 A; 2883 C; 2734 G; 2079 T; 0 other;

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| 5.1.6 Compugen Ltd. | | ; Search time 1859.96 Seconds (without alignments) 9447.586 Million cell updates/sec | TACTCTTTGCTCCCTAATAG 723 | | dues | rs: 45562784 | | | | | | | | | | | | | | | results predicted by chance to have a 1 to the score of the result being printed, of the total score distribution. | | Description | AV755731 AV755731 AV758366 AV758366 AV758366 BI879124 £m04e08.y AV835132 AV835132 |
| GenCore version 5. Copyright (c) 1993 - 2003 Co | OM nucleic - nucleic search, using sw model | Run on: December 19, 2003, 18:03:34 ; S (wit) | Title: US-09-899-303A-21 Perfect score: 723 Sequence: 1 ATGTTGGGTAAGGTCATCGA | Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0 | Searched: 22781392 segs, 12152238056 residue | Total number of hits satisfying chosen parameters | Minimum DB seq length: 0 Maximum DB seq length: 2000000000 | Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries | Database : BST:* | 1: em_estba:* 2: em_estba:* 3: em_estpa:* | 4: em estmu:* 5: em_estov:* | | 9: gb_est:* 10: gb_est2:* 11: gb_est2:* | 12: 9D_e8t3:* 13: 9D_e8t4:* 14: or best 5:* | 15: em_estfun:* 16: em_eston:* | 17: em_gss_hum:* 18: em_gss_inv:* 19: em_gss_pln:* | | 22: em_gss_mam:* 23: em_gss_mus:* | | | Pred. No. is the number of results predicted score greater than or equal to the score and is derived by analysis of the total stands. | SUMMARIES | Result Query No. Score Match Length DB ID | c 1 101.2 14.0 488 9 AV755731 c 2 79.6 11.0 492 9 AV758366 c 3 41.6 5.8 502 12 BI879124 4 40.6 5.6 275 9 AV835132 |

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BI879124
BI879124.1 GI:16086395
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,

Gu,Y., Li,N., Qian,B., Liu,F., Qu,V., Gao,K., Cheng,Z., Xu,Z., Zeng,J., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G.,

Yang, Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z.

Homo gapiens CDNA BM clones
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/db_xre="laxon:960"
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/note="Vector: pTriplEx2; Site_1 = 4 others
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Contact: Zequang Han
Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
Tel: 86-21-50801999 (ex.45)
Fax: 86-21-50801992
Email: hansgéorher.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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/mol_type="mRNA"
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AV758366 BM Homo gapiens cDNA clone BMFAKA03 5', m
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Caniata; Ostariophysi; Cypriniformes Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 502)

2 (lark, M., Johnson, S.)

3 Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Rohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Wabhi Zebrafish EST Project 1998
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
7Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrasfish@watson.wustl.edu
Email: zbrasfish@watson.wustl.edu
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Sequencing by: Washington University Genome Sequencing Center Clone
Astribution: ReseaucenZentrumPrimarDatenbank, Berlin, Germany
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
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/dev stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare_subsp. spontaneum top three leaves adult, heading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484 GOCCATGAGCATGAGCCACCACATGATGGCATGGTTTCGCCAGACCGAAAGTTGTTG 425
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AV835132 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
spontaneum top three leaves adult, heading stage Hordeum vulgare subsp. spontaneum cDNA clone bah24018, mRNA sequence.
AV835132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 GGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCG
/ Beks "usacu"
/ dev stages"1-2 years"
/lab_host=="1-2 years"
/lab_host=="E.Coli XLI-Blue MRF')"
/clone lib=Zebrafish adult retina cDNA"
/note="Vector: Lambda ZAP II (pBluescript SK-); Site_BCORI; Site_2: Sall; This Zebrafish library was constructed by Dr. Susan B. Brockerhoff (email: sbrocker@u.washington.edu) RZPD library number: 760"
a 163 c 125 g 116 t
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        Length 502;
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Pred. No. 4.4;
0; Mismatches
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/clone="bah24018"
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/cultivar="H602"
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402 bp mRNA linear EST 23-APR-2002 AV392783 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii AV392783 AV392783
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/strain="C9"
/db.xref="tcaon:3055"
/clone="CM096g04_r"
/dev_stage="photoautotrophic growth"
/clone lib="Chlamydemonas reinhardtii C9"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
A large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
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Length 275;
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/organism="Chlamydomonas reinhardtii"
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342 GGAGAACAACTCTTCCCGCTGCTGGGT 368
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Location/Qualifiers
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DCMB Box 91000
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGG 161
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadacae; Chlamydomonas.
Chlamydomonadacae; Chlamydomonas.
Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
A large scale structural analysis of cDNAs in a unicellular green
alga, Chlamydomonas reinhardtii. I. Generation of 3433
and-redundant expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
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/dlone="CM083e05_r"
/dev stage="photorophic growth"
/dlone lib="Chlamydomonas reinhardtii C9"
/dlone lib="Totor: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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/mol type="mRNA"
/strain="C9"
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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288 CTTCGCCGTCCGCTGCGTGGGCCACTCGCTGGCGGCGGCGCCCCCGCCGGCTGCCTGTCGAT 347
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Chlamydomonas reinhardtii
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Enhamydomonadaceae; Chlamydomonas.
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Grossman, A., Chang, C., W., Davies, J., Harris, E., Hauser, C., Lefebvr
F., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
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/strain="CC-1690 wild type mt+ 21gr"
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Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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                                                                                                                    BI727879
1031095C12.yl C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Location/Qualifiers
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DCMB Box 91000
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
/note="lst strand cDNA was primed with a NotI-oligo(dT)
/note="lst strand cDNA was primed with a NotI on Section contains of the pCMVSPORT 6 vector. Library was normalized."

88 c 93 g 398 t 506 others
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Genoscope - Centre National de Sequencage
Branta 191006 EVRY cedex - France
Brail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
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Query Match 5.6%; Score 40.6; DB 12; Best Local Similarity 45.3%; Pred. No. 8.4; Matches 148; Consérvative 0; Mismatches 179;
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AGENCOURT_6611605 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5485649
5', mRNA sequence.
BM918259
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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               GECTICGCCGACCICGTGGGGTACATICCGCTCGICGGGGCCCCCCTAGGGGGCGCTGCC 93
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Email: cgapbs-r@mail.nih.gov
Tissue procurement: Dr. Daniel McVicar, DBS/NCI
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2016 row: n column: 18
High quality sequence stop: 567.
                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                      94 AGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAACTATGCAACAGGAAT
                                                                        678 SSSSSSBBITITSSSTSSSSTISSSTISSSTTTTTTSBTSSSTSBSBTTSCTT
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/note="wetor" pcmvsport 6; lst strand cDNA was primed
/note="wetor" pcmvsport 6; lst strand cDNA was digested with Not I and cloned into
double-strand cDNA was digested with Not I and cloned into
the Not I and BcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

library was not normalized."

11 a 311 c 349 g 146 t. 194 others
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 9100 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4924.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
France Library BEA11: fliang@lifetech.com URL:
France BP BEA11: fliang@lifetech.com URL:
France Faraday Avenue Genoscope sequence ID: CLOBA006ZG08RPI.
Faraday Avenue Genoscope sequence ID: CLOBA006ZG08RPI.
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/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2: ECRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRIXAhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Upublished
On Feb 13, 2001 this sequence version replaced gi:12777380.
Contact: Genoscope
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Pred. No. 13;
0; Mismatches 68;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases 1 to 375)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
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                                                              297 CTTCAAGTGCAACAGCGCCGTCTGGAAGGCGCTCAGGGCGGTCGACGCCGTCGCCGTCGG 238
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                        83
                                                                                                   84 GGGCGTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGACGCGTGAACTATG 142
                                                                                                                              237 GGACGCCGGCAGCCCCTGGGCGCAGGACGTGCTGCCGGTGCACGTGCCCAAGG 179
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                      CCTTACATGCGGCCTTCGCCGACCTCGTGGGGGTACATTCCGCTCGTCGGCGCCCCCCTAGG
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/clone="wh55919"
/tissue type="spike at flowering date"
/dev_stage="Peekes' scale 10.5.1"
/clone lib="Y. Ogihara unpublished cDNA library, N
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Conter For Genetic Resource Information
National Institute of Genetics
1111 Yata, Wishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Triticum aestivum
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BJ252669 Y. Ogihara unpublished cDNA library, Wh_f Triticum
aestivum cDNA clone whf25g19 3', mRNA sequence.
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1 (bases 1 to 359)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished
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/dev_stage="Feekes' scale 10.5.1"
/clone_lib="Y. Ogihara unpublished cDNA library,
i 115 c 107 g 67 t
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  DB 9; Length 1201;
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58.0%; Pred. No. 18;
tive 0; Mismatches 50; Indels
Query Match 5.5%; Score 40; DB 9; Length 120 Best Local Similarity 26.5%; Pred. No. 15; Matches 103; Conservative 104; Mismatches 179; Indels
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Tel: 81-559-81-6856
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Center For Genetic Resource Information
National Institute of Genetics
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whf25919"
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Location/Qualifiers
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Matches 69; Conservative
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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    Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budinan, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
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Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
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EL01T0207811.b Endosperm_4 Zea mays CDNA, mRNA sequence
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                                                                                                        Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing of the maize endosperm ESTs
Unpublished
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/mol_type="mRNA"
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                                                                    Unpublished
Contact: Cathy Whitelaw
(bases 1 to 840)
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   /db_xref="taxon:4577"
/db_xref="taxon:4577"
/close_lib="Endosperm_4"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
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ALIGNMENTS

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US-Gequence 21, Application US/08612973
| Sequence 21, Application US/08612973
| Patent No. 6150134
| General Liferbandion US/08612973
| Patent No. 6150134
| General Liferbandion US/08612973
| Patent No. 6150134
| APPLICANT: BOSHAN FONS
| APPLICANT: BOSHAN FONS
| APPLICANT: BOSHAN FONS
| APPLICANT: BUYSE, MARIE-ANGE
| TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
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| TELEFAX: (703) 816-4100
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                CITY: ARLINGTON
STATE: VIRGINIA
COMPUTER: U.S.A.
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1100 NORTH GLEBE ROAD
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
IENGTH: 723 base pairs
TYPE: nucleic acid
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Matches 723; Conservative
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APPLICANT: MESTERS, FONS
APPLICANT: BOSWAN, FONS
APPLICANT: BUSBAN, FONS
APPLICANT: BUYSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: 11
CORRESPONDENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                         .
0
                                                  Length 723;
                                                     100.0%; Score 723; DB 3; Length 7
100.0%; Pred. No. 2.5e-183;
tive 0; Mismatches 0; Indels
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Patent No. 6245503
GENERAL INFORMATION:
                                                               100.
Best Local Similarity 100.
Matches 723; Conservative
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                                                                                                      Gaps
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                                                                  Score 641; DB 3;
Pred. No. 1.7e-161;
0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
                                                                  Query Match
Best Local Similarity 90.9%;
Matches 723; Conservative
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mat peptide
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   ; NAME/KEY:
; LOCATION:
US-08-612-973-5
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US-08-927-597-5
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                                                                 CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08612973

Batent No. 6150134

GENERAL INFORMATION:

APPLICANT: MAERTENS, GERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUSNEN, FONS
APPLICANT: BUYSE, MAITE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF SEQUENCES: 111
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ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSFIECATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
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STRANDEDNESS:
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FEATURE:
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LOCATION:
FEATURE:
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US-08-612-973-5
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301 GACATGATCATGCACCCCCGGGTGCGTGCCTGCGTTCGGGAGAACAACTCTTCCCGC 360
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APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: 1100 NORTH GLEBE ROAD
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PALENTIN Release #1.0, Version #1.25 (EPO)
SOFTWARE: PALENTIN Release #1.0, Version #1.25 (EPO)
SOFTWARE: PALENTIN NORTH: 32,205
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 32,205
REGISTRATION INFORMATION:
NAME: BYRNE, THOMAS E: 32,205
REGISTRATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
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TELEPHONE: (703) 816-4100
TELEPHONE: LENGTH: EBORDENERS
LENGTH: Z082 DASS PALES
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                                                                                                                                                                                                                       421 ATACGACGCCACGTCGAT-----
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Patent No. 6150134
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         439 -----
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US-08-612-973-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCGCTTATGAAGTGCGCAACGTG 240
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                                             APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
STREET: 1100 NORTH GLEBE ROAD
STREET: VINGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
APACHETANENTON.
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90.9%; Pred. No. 1.7e-161;
ive 0; Mismatches 0;
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CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4100
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TELEFAX: (703) 810-4100
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Best Local Similarity 90.9
Matches 723; Conservative
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, LOCATION:
US-08-927-597-5
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INFORMATION FOR SEQ ID NO: 47
SEQUENCE CHARACTERISTICS:
LENGTH: 2082 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                     GENERAL INFORMATION:
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FEATURE:
NAME/KEY: CDS
LOCATION: 1..2
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HYPOTHETICAL: N
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; LOCATION:
US-08-927-597-47
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                                                                                                                                                                                                                                                                                                                                                                             CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG 123
                                                                                                                                                                                                                                                                                                                                                                                                 64 CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGATGGCGTCCGGGTTCTG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 GAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 GAGGACGCGFGAACTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGGCTTIGCTGTCCTGTCTGACCGTTCCGGCTTCCGCTTATGAAGTGCGCAACGTGTCC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 ATGATCATGCACACCCCGGGTGCGTGCCTTCGGGAGAACAACTCTTCCCGCTGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 ATGATCATGCACACCCCCGGGTGCCTGCCCTTCGGGAGAACAACTCTTCCCGCTGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACAATA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 CGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544 GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              664 CGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCCATTGGGGAGTCCTGGCGGGC 723
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                                                                                                                                                                                                                                                                                                                           4 TIGGGTAAGGTCAICGAIACCCTIACAIGCGGCTTCGCCGACCTCGTGGGGTACATTCCG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 GACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         604 GCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 GCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
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                                                                                                                                                                                                                                                                                                          TTGGGTAAGGTCATCGATACCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATTCCG
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                         72;
                                                                                                                                                                                                                                           Length 2082;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                      Score 624.8; DB 3;
Pred. No. 4.7e-157;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 CGACGCCACGTCGAT-------
                                                                                                                                                                                                                                        86.4%;
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.5
Matches 708; Conservative
                                                                                                                                                                     mat_peptide
TYPE: nucleic acid
STRANDEDNESS: single
                                TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                  1..2079
                                                                                ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 -----
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                                                                                                                                                | FEATURE:
| NAME/KEY: |
| LOCATION:
| US-08-612-973-47
                                                                                                                                    LOCATION:
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CGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGCGGGT 651
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Best Local Similarity 90.5%; Pred. No. 4.9e-157;
Matches 708; Conservative 0; Mismatches 2;
ATTORNEY/AGENT INFORMATION:
NAME: BFRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 1487-
TELECOMMINICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2433 base pairs
TYPE: nucleic acid
STRANDEDNES: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ANTI-SENSE: NO
FEATURE:
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; LOCATION:
US-08-612-973-49
                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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                                                                                                                                                           304 ATGATGATGACGCCCCGGGGTGCGTGCCTTGCGGTAGAACAACTTCTTCCCGCTGC 363
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                                            184 riddciriidcidiccidicidaccdiiccadcriccacriardaaGraccaacGrafcc 243
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APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUSE, MARTYNOFF, MARTE-ANGE
APPLICANT: BUYES, MARTE-ANGE
TITLE OF INVENTION: PROTEINE FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COMPUTER: READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPILCATION DATA:
APPLICATION UNDER: 11. MS PC-DOS/MS-DOS
SOFTWARE: 11. MS PC-DOS/MS-DOS

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Patent No. 6150134
GENERAL INFORMATION:
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US-08-612-973-49
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         355 TTGGGTAAGGTCATCGATACCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATTCCG 414
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                                                 64 CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG
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Fatent No. 6150134
GENERAL INFORMATION:
APPLICANT: BOSMAN, FONS
APPLICANT: BUSSE, MARIE-ANGE;
APPLICANT: BUYSE, MARIE-ANGE;
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEB: NIXON & VANDERHYE P.C.
STREET: 11100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 CGACGCCACGTCGAT-----
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STATE: VIRGINIA
COUNTRY: U.S.A.
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US-08-612-973-25
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                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTFIED FOR DIAGNOSTIC AND THERAPEUTIC USE
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ANDRESS:
CORRESPONDENCE NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
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Pred. No. 4.9e-157;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                     Sequence 49, Application US/08927597
Patent No. 6245503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1.
TELECOMMUNICATION INFORMATION
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90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEO ID NO: 49
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2433 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 90.5
Matches 708; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIRGINIA
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                                                                                                                                                                                             GC 1136
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                                                                                                                                                    712 GC 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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LOCATION:
US-08-927-597-49
                                                                                                                                                                                                                                                            RESULT 8
US-08-927-597-49
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541 ATGATGATGATCGCTCTCGCCTACAACGGCCCTGGTATCGCAGCTGCTCCCGGATCCCA 600
                                  1 ATGITGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGGTACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BORMAN, FOND
APPLICANT: BORMAN, FOND
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PURIFIED HERATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PURIFIED HERATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
ADDRESSEE: ADDRESS: ADDRESS: ADDRESSEE: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTIBLE OF COMPUTER: DEADABLE FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/927,597

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

82.7%; Score 598.2; DB 3;
Best Local Similarity 99.5%; Pred. No. 3.8e-150;
Matches 600; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/612,973
APPLICATION NUMBER: US 08/612,973
BILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
INFORMATION FOR SEO ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 DASE pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                 sequence 25, Application US/08927597; Patent No. 6245503; GENERAL INFORMATION: APPLICANT: MARRIENS, GERRT APPLICANT: BOSMAN, FONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: mat_peptide
; LOCATION: 1..600
US-08-927-597-25
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STATE: VIRGINIA
COUNTRY: U.S.A.
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LOCATION: 1...
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MOLECULE TYPE:
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ANTI-SENSE: NO
FEATURE:
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                                                                                                                                       601 CAA 603
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                                                                                                                                                                                                                                                                                           RESULT 10
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ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
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99.5%; Pred. No. 3.8e-150;
cive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.5
Matches 600; Conservative
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MOLECULE TYPE: CD
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LOCATION:
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, LOCATION:
US-08-612-973-25
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100.0%; Pred. No. 8.2e-150;
iive 0; Mismatches 0;
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US-08-927-597-27
; Sequence 27, Application US/08927597
; Patent No. 6245503
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
  *** TELEFAX: (703) 816-4000

TELEFAX: (703) 816-4000

**** INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SPRNE
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Matches 597; Conservative
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                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
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CCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT 120
                                                                               CTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTC 180
                                                                                                     CTGGAGGACGACGTGAACTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTC 180
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                              CCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGTTGGCGTCCGGGGTT
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APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUSENAN, FONS
APPLICANT: BUSEN, MARRYNOFF, GUY
APPLICANT: BUSEN, MARRYNOFP, GUY
APPLICANT: BUSEN, MARRYNOFP, GUY
APPLICANT: BUSEN, MARRYNOFP, GUY
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E:
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-612-973-27
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481 CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT 540
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APPLICANT: BUSINANTE-MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin NG-086 12,973
FILING DATE: 11-MAR-1996
CLASSIFICATION NUMBER: U3/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION NUMBER: 32,205
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
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Sequence 23, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MAERTENS, GEERT APPLICANT: BOSMAN, FONS
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Best Local Similarity
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ANTI-SENSE: NO
FEATURE:
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LOCATION:
US-08-612-973-23
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                            APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
APPLICATION NUMBER: US/08/927,597
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82.6%; Score 597; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 8.2e-150;
Matches 597; Conservative 0; Mismatches 0;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 11-WAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 1487-10
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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LOCATION:
US-08-927-597-27
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COUNTRY:
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61 CCGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT 120
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Pred. No. 6.4e-139;
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100.0%; Pred. No. e...
0; Mismatches
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US-08-470-426B-17
; Sequence 17, Application US/08470426B
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNEY. THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1497-
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE STARATICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity 100.(
Matches 556; Conservative
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LOCATION:
FEATURE:
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LOCATION:
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                                              1 ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT
        Gaps
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Patent No. 6245503

GENERAL INFORMATION:
APPLICANT: MARRTENS, GERT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: NIXON & VANDERHYE P.C.
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0
                                                                                                                                                                                                   CTGGAGGACGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCT
        0; Indels
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMpatible
COMPUTER: BATCHITH Release #1.0, Version #1.25 (EPR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
        Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
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US-08-927-597-23
        256;
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Search completed: December 20, 2003, 07:03:07
Job time : 56.1425 secs
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Patent No. 5856458
GENERAL INFORMATION:
APPLICANT: Okamoto, Hiroaki
APPLICANT: Nakamura, Tetsuo
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B
TITLE OF INVENTION: HEPATITIS VIRUS
NUMBER OF SEQUENCES: 33
CORRESPONDENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGGGIAGCGCICACCCCCACGCICGCAGCIAGGAACGCCAGCGICCCCACCACGACAAIA 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 549.6; DB 2; Length 1539;
Pred. No. 4.4e-137;
0; Mismatches 49; Indels 72;
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPATING SYSTEM: PC-DOS/WS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,426B

FILING DATE: 06-JUN-1995

FILING DATE: 12-UNN-1990

ATTORNEY/AGENT INFORMATION:

ANAMER: 12-UNN-1990

ATTORNEY/AGENT INFORMATION:
                                                                                                                                        ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young, ADDRESSEE: L.L.P. STREET: 1850 M Street, N.W., Suite 800 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Weilacher, Robert G.
REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06/59-47083.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.0%;
Best Local Similarity 84.5%;
Matches 661; Conservative <sup>0</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 659-2811
TELEFAX: (202) 659-1462
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1539 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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December 19, 2003, 16:55:48; Search time 2124.1 Seconds (without alignments) 10804.703 Million cell updates/sec
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561
1 ATGITGGGTAAGGTCATCGA......TGATGATGAACTGGTAATAG 561
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                       2888711 segs, 20454813386 residues
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Maximum Match 100%
Listing first 45 summaries
                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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SUMMARIES

| | Description | A48685 See A48685 See A48681 See A48681 See A48681 See A48681 See A48681 See A48681 See A48681 See A48681 See A48681 See A48681 See A48681 See A48681 See A48681 See A48681 See A48681 See A48861 See A48681 See | PROTEINS FOR DIAGNOSTIC AND |
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100.0%; Pred. No. 2e-118;
Live 0; Mismatches 0; Indels
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Sequence 23 from patent US 6245503.
AR157337 GI:16218270
         Other publication CA 2172273 960215
Other publication AU 3382495 960304.
Location/Qualifiers
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
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Sequence 23 from Patent BP1211315.
AX452772
                                                                                            therapeutic use
Patent: US 6245503-A 23 12-JUN-2001;
Location/Qualifiers
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AUTHORS
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                                                                           Maertens,G., Bosman,P. and Buyse,M.A.
Purified Hepatitis C Virus envelope proteins for diagnostic therapeutic use
Patent: WO 0.2055548-A 23 18-JUL-2002;
INNOGENETICS N.V. (BE)
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses,
Hepacivirus.
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Recombinant vectors for producing hov envelope proteins Patent: EP 1211315-A 23 05-JUN-2002; Innogenetics N.V. (BE)
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| codon start=1
| protein id="CDA03136.1"
| db_xref="G1:2302401"
| translation="MIGKVIDTLITGFADLVGYIPLVGAPLGGAARALAHGVRVLEDG
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| IMMTPECCVPCWRENNSSRCWVALITPTLAARRARANSVPTTTIRRHVDSQLFTISPRRHETV
| QDCNCSIYPGHITGHRMAWDMWMWSPTTALVVSQLRRIL"
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unclassified.

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Mactens, G., Bosman, F., De, M.G. and Buyse, M.

Mattens, G., Bosman, F., De, M.G. and Buyse, M.

PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THEARABUTIC USB

INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 382495 960304.

Cher publication AU 382495 960304.

Location/Qualifiers

I. 606

/organism="unidentified"
/mol_type="genomic DNA"
/d D_xref="taxon:32644"
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QDCNCSIYPGHITGHRMAWDWMMWSPTTALVVSQLLRIL"
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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       421 ATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTG
                                         481 CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT
                                                            481 CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT
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/organism="Hepatitis C virus"
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Best Local Similarity 100.0%; Pred. No. 2.8e-117;
Matches 556; Conservative 0; Mismatches 0;
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Patent: WO 02055548-A 25 18-JUL-2002;
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Location/Qualifiers
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QDCNCSIYPGHITGHRWAWDMWMNWSPTTALVVSQLLRIL"
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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/organism="Hepatitis C virus"
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1. .603
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Sequence 25 from Patent EP1211315.
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1 (bases 1 to 636)
Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
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241 TCCGGGATGTACCATGTCACGAACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
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larity 100.0%; Pred. No. 2.8e-117;
Conservative 0; Mismatches 0;
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Patent: US 6245503-A 27 12-JUN-2001;
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/db xref="G1:2302403"
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QDCNCSIYPGHITGHRMAWDNWMNWSPTTALVVSQLLRIVIEGRHHHHHH"
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B Haetens, G., Bosman, F., De, M.G. and Buyse, M.

Raetens, G., Bosman, F., De, M.G. and Buyse, M.

PURIFIED HEAPTITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND PURIFIED HEAPTITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND PURICE USE

I Patent: WO 9604385-A 27 15-FEB-1996;

INNOCRNETICS NV (BE)

Other publication AU 3382495 960304.

Other publication AU 3382495 960304.

L. 636

/ Organism="unidentified"

//mol type="genomic DNA"

//mole="unnamed protein product"
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99.1%; Score 556; DB 6; Length 63
Best Local Similarity 100.0%; Pred. No. 2.8e-117;
Matches 556; Conservative 0; Mismatches 0; Indels
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Sequence 27 from Patent WO9604385.
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/db_xref="G1:29371434"
/db_xref="G1:293714"
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    CTCTTGGCTTTGCTGTCCTGTCTGACGGTTCCAGCTTCGGCTTATGAAGTGCGCAACGTG
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Purified Hepatitis C Virus envelope proteins for diagnostic
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Local Similarity 100.0%; Pred. No. 2.8e-117; es 556; Conservative 0; Mismatches 0;
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/note="unnamed protein product"
/codon_start=1
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses,
Hepacivirus.
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Patent: WO 02055548-A 27 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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Sequence 27 from Patent W002055548.
AX685028
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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IMHTPGCVPCVRENNSSRCWVALTPTLAARNASVPTTTIRRHVDSQLFTISPRRHETV
QDCNCSIYPGHITGHRMAWDMMNWSPTTALVVSQLLRIVIEGRHHHHHH"
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Pred. No. 2.8e-117;
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/mol type="genomic DNA"
/db_xref="taxon:11103"
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/note="unnamed protein product"
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1 (bases 1 to 723)

Metrens, G., Bosman, F., De, M.G. and Buyse, M.

PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND PARTHER WOOD 9604385—A 21 15-FEB-1996;

INNOGENETICS NV (BE)

Other publication CA 2172273 960215

Other publication AU 3382495 960304.
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/db xref="G121712456"
/translation="MLGKVIDTLTCGFADLVGYIPLVGAPLGGAARALAHGVRVLEDG
VNYATGNLPGCSFSIFLIALLSCLTVPASAYEVRNVSGAYTHVTNDCSNSSIVYEADM
IMHTPGCVPCVRENNSSRCVVALITPTLAARNASVPTTTRRHVDSQLFTISPRRHETV
QDCNCSIYPGHITGHRAANDMANNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGL
AYYSMVGNWAKVLIVMLLFAP.
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; huma
serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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AAV42305
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Hepatitis C virus Fragment of NANB h Hepatitis C virus HCV-S1 full-length

vaccine; human;

Maertens G;

Score

Result Š.

AAL48926 standard; DNA; 561 BP

(first entry)

24-OCT-2002

AAL48926;

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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1 and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1. E2, and E1/E2 proteins. C in vectors for the production of recombinant E1. E2 and E1/E2 proteins. C invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known
proteins - in presence of dissulphide bond cleavage agent, to
produce proteins suitable for direct use in vaccines or diagnostic
assays of HCV
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Sequence 561 BP; 103 A; 176 C; 155 G; 127 T; 0 other;

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181 CICITGGCITTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGAACGTG

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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV El and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to invitro molitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                                                                                                                                                                                                 Hepatitis C virus clone HCCI38 B1 protein coding sequence.
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                                                                                                                                                                                                                                                                                           Hepatitis C virus, HCV, El protein, E2
                                                                                                                                                                                                                                                                                                                           virucide; immunostimulant; vaccine;
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30-AUG-2001; 2001US-315768P.
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into a reversed phase hybridisation assay for determining the presence the genotype of HCV. The new purfication method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT
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                                                                                                                                                                                                                                              99.1%; Score 556; DB 17; Length 606; 100.0%; Pred. No. 1.2e-138; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus clone HCCI39 El protein coding sequence
                                                                                                                                                                                                Sequence 606 BP; 109 A; 193 C; 167 G; 137 T; 0 other;
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Matches 556; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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es 556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 556; DB 24; L Pred. No. 1.2e-138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%; Scor. 100.0%; Pred. No. 1... 0; Mismatches
                                                                                                                                                                                                                                                   Example 2; Page 177-178; 243pp; English.
                                                                                                   Buyse M;
11-JAN-2002; 2002WO-EP00219.
                            11-JAN-2001; 2001US-260699P
30-AUG-2001; 2001US-315768P
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                                                                         (INNO-) INNOGENETICS NV
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556; Conservat
                                                                                                                                   WPI; 2002-599657/64
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Matches 556;
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1 cand E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. Cr in vectors for the production of recombinant E1, E2, and E1/E2 proteins. Cr invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out cleavage agent, after 19sis of recombinant host cells. Cr invention to constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a sercityping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence of the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and conformation of the recombinantly expressed E1, E2 and E1/E2, and are more reactive with human sera than those isolated by known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic
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                                     95WO-EP03031.
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or B2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for ratising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                                                                                                                                                                                                         GACATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGGAGAACAACTCTTCCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus clone HCCI40 El protein coding sequence.
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30-AUG-2001; 2001US-315768P.
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AATI2704-T12709 and AATI2961-T12974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the cinvention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a contructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detecting one or antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated contour search phase hybridisation mested preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and conformation of the recombinantly expressed E1, E2 and E1/E2, and conformation envelope proteins. Antigens isolated by known
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purifying recombinant hepatitis C virus (HCV) E1 and E2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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99.1%; Score 556; DB 17; Length 7

Best Local Similarity 100.0%; Pred. No. 1.3e-138;

Matches 556; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              Maertens
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                                                    Hepatitis C virus.
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligometric recombinant envelope proteins selected from an El and specific oligometric recombinant envelope proteins selected from an El and seful for inducing HCV-specific antibodies or for immunising humans useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV El and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                                                                                                                    CAGGACTGCAATTGCTCAATCTGGGCCACATAACGGGTCACCGTATGGCTTGGGAT
                                                                            TGCTGGGTAGGGCTCACCCCCACGCTAGGAACGCCAGGGTCCCCACCACGACA
                 ATACGACGCCACGTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTG
                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; El protein; E2 protein; infection; gene; virucide; immunostimulant; vaccine; ds.
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                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus clone HCCI37 E1 protein coding sequence.
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P-PSDB; AAO18666.
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Best Local Similarity
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                                                                                             CTGGAGGACGGCGTGAACTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-129401/13
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant El, E2, and El/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage agent, after 1943 of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed El, E2 and El/E2, and eliminates contaminating proteins. Antigens isolated using this method are mer more reactive with human sera than those isolated by known
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                         agent, to
or diagnostic
    E2 envelope
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Purifying recombinant hepatitis C virus (HCV) El and protetins - in presence of di:sulphide bond cleavage produce proteins suitable for direct use in vaccines assays of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 795 BP; 130 A; 240 C; 231 G; 194 T; 0 other;
                                                                                                             Claim 23; Fig 21; 146pp; English
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481 GGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGG

529 ATGGCTTGGGATATGATGATGAACTGGT 556

CATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCGGGCCACATAACGGGTCACCGT

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30-AUG-2001; 2001US-315768P.
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P-PSDB; AAO18678.
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                                                                                                                                                                       E2 protein; infection; gene; ds.
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84.5%; Score 474; DB 24; Length 795;
Best Local Similarity 88.5%; Pred. No. 1e-116;
Matches 556; Conservative 0; Mismatches 0; Indels 7
                                                                                                                                                  Hepatitis C virus clone HCCI10A El protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 795 BP; 130 A; 240 C; 231 G; 194 T; 0 other;
              601 ATGGCTTGGGATATGATGATGATGAACTGGT 628
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30-AUG-2001; 2001US-315768P.
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a
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                                                                                                                                                                                                                                                                                                                                                  469 CATGAGACGGTGCAGGACTGCAATTGCTCAATCCTGGCCACATAACGGGTCACGT
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                                                                     GACATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGAGAACAACTCTTCCCGG
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composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an E1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                                                                                                                                                                                                      Score 471; DB 24;
Pred. No. 8.4e-116;
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HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human;

standard; DNA; 2086

AAT12973

AAT12973

(first entry)

24-SEP-1996

#X#X#X#X

HCV El construct HCC165

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and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant E1, E2, and E1/E2 proteins. The recombinant proteins on then be isolated using a method of the invention. In the method, the envelope proteins are purified by a carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and are more reactive with human sera than those isolated using this method are more reactive with human sera than those isolated by known
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serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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Pred. No. 8.4e-116;
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                                                                                                                                                                                                                                                                                                                                                                  7;
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the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCGGGCCACATAACGGGTCACGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 GGGATGTACCATGTCACGAACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 TIGGGIAAGGICAICGATACCCTIACAIGCGGCTTCGCCGACCTCGTGGGGTACAITCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGGTACATTCCG
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                                              Length 2433;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                       Sequence 2433 BP; 434 A; 745 C; 714 G; 540 T; 0 other;
                                                                                                                                                                                                                                                                                                  Score 471; DB 17;
Pred. No. 8.8e-116;
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88.5%;
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Best Local Similarity 88.5
Matches 553, Conservative
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WPI; 2002-599657/64.
P-PSDB; AAO18662.
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                                                                                                                                                                                                                                                                   AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1 and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction of HCV constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are mer meter ereactive with human sera than those isolated by known
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                              Purifying recombinant hepatitis C virus (HCV) E1 and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.2%; Score 461.4; DB 17; Length 633; llarity 86.9%; Pred. No. 2.2e-113; Conservative 0; Mismatches 11; Indels 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 633 BP; 111 A; 192 C; 174 G; 156 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                              De Martynoff G,
                                                                                                                                                                                                                                                Claim 23; Fig 21; 146pp; English
                                                                          94EP-0870132
                                                   95WO-EP03031
                                                                                                    (INNO-) INNOGENETICS
                                                                                                                              Виуве М,
                                                                                                                                                      WPI; 1996-129401/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
Les 550; Conserv
                                                                          29-JUL-1994;
WO9604385-A2
                                                   31-JUL-1995;
                         15-FEB-1996.
                                                                                                                              Bosman F,
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition contraining at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an E1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to
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                                                                                                                                                                                                                                                                     541 CATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACAGGTCACCGT
421 ATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTG
                                                                                                                                                  481 GGGGATCTCGCGGATCTGCTCTCCTCTCCAGCTGTTCACCATCTCGCCTCGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; El protein; E2 protein; infection; gene; virucide; immunostimulant; vaccine; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus clone HCCI11A El protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E patients suffering from HCV infection. The F sequence described in the exemplification of
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86.9%; Pred. No. 2.2e-113;
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| els | CCTCGT | CCTCAT | SCATGE | GCATG | CTCTT | CTCTT | TGAAG | TGAGG | TGTGT | TGTĞT | GAACA | GAACA | CGTCC | CAGCGTCC | | STTCCG | CATCT | CCATCT | ACATAA | ACATAA | | |
| Indels | GCCGA | GCCGA | CTGGC | CTGG | GGTTG | rccrrc | GCTTA | CGCTTA | AAGCAT | AAGCAT | TCGGGA | rceeca | CGCCAG | ceccae | | TITCL | -rcccagcrgrrcaccarcrcgcrr | GTTCA | CGGCC | COOCC | | |
| 11; | GGCTTC | GGCTTC | AGGGCC | AGAGC | TTGCCC | Tracci | GCTTC | GCTTC | PACTO | AACTC | TGCGT | TĠĊĠŢ | FAGGAA | raggaa | | GCTGC | CCAGCT | ccacci | CTATC | CTATC | G 561 | Ġ 633 |
| Mismatches | ATGTTGGGTAAGGTCATCGATACCTTACATGCGGCTTCGCCGACCTCGTGGGGGTACATT | ATGTTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATT | CCGCTCGTCGCCCCCCTAGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT | cogracoscocccccanogososososososososososososososososososo | CTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTC | CIGGAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTTTC CTGGAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTTTCTT | CTTTGCTGTCCTGTCTGACGTTCCAGCTTATGAAGTGCGCAACGTG | <u>ciriescitiaciercecererceacerrececerrargaggrecentatargaggreceracere</u> | TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGGATTGTGTATGAGGCAGCG | <u>receggatgtaccatgtcacgaacgactgctccaactcaagcattgtgtatgaggcagcg</u> | GACATGATCATGCACCCCGGGTGCGTGCGTCGCGTTCGGGAGAACAACTCTTCCCGC | | TGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACACA | <u>rgcragaragcacrcaccccacacrcacaacacac</u> | 1 | | DI | gasarcressarcracrescesses | CATGAGACGGIGCAGGACTGCAATGCICAATCTATCCCGGCCACATAACGGGTCACCGT | CATGAGACGGTGCAGGACTGCAGTTGCTCAATCTATCCGGGCCACATAACAGGTCACCGT | ATGGCTTGGGATATGATGATGAACTGGTAATAG | ATGGCTTGGGATATGATGATGAACTGGTAATAG |
| Misma | CCCTT | CCCTT | 3GGGGC | GGGGT | SCAACA | SCAACA | CTGACC | CTGACC | AACGAC | AACGAC | GGGTGC | geerge | ACGCTC | ACGCTC | | CTCGT | | TTCCT | AATTG | AATTG | SAACTG | SAACTG |
| 0; | TCGAT | TCGAT | CCCTAC | CCCTA | ACTAT | ACTAT | CCTGT | ccrer | STCACG | TCACG | ACCCCC | ACCCCC | ACCCC | ACCCCC | GAT | GATTTC | | TCTGT | GACTG | GACTG | ATGAT | ATGAT |
| ative | AGGTCA | AGGTCA | 300000 | 300000 | GCGTGA | GCGTGA | TGCTGT | racre | ACCATO | ACCATO | TGCAC | TGCAC | CGCTC | CGCTC | ACGTC | ACGTO | | rgcgga | STGCAG | GTGCAG | SATATG | GATATG |
| Conservative | GGGTA | GGGTA | CGTCG | CGTCG | GGACG | AGACG | GGCTT | GGCTT | GATGT | GATGT | IGATCA | TGATCA | GGGTAG | GGGTAG | ATACGACGCCACGTCGAT | GACGC | | ATCTC | AGACG | AGACG | CTTGG | CTTGG |
| | ATGTT | ATGTT | CCGCI | | _ | CTGG/ | 5- | _ | - | - | _ | - | | | | | 6 | | _ | | | |
| 550; | 7 | н | 61 | 61 | 121 | 121 | 181 | 181 | 241 | 241 | 301 | 301 | 361 | 361 | 421 | 421 | 435 | 481 | 469 | 541 | 529 | 601 |
| Matches | | | | | | | | | | | | | | | | | | | | _ | | • |
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Search completed: December 19, 2003, 18:51:15 Job time : 158.093 secs

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Run on:

Sequence:

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Homo sapiens
Bukaryota, Marazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)
Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,
Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng, L., Xu,S., Gu,W., Tu,Y., Jia,J., Pu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z., Unpublished
                                                           BL7278791 1031095C1
BX35664 BX356664
BW91825 AGENCOURT
AL513886 AL513886
BU725669 BJ752669
BU725669 BJ752669
BU725669 BJ752669
BU725616 BJ746716
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BU73510 BC09Dh11
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AL09878 Drosophil
AL19277 Drosophil
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CC010088 PUHRD18TB
CC405164 PUHSF17TB
BC735026 PUHRD18TB
CC359026 PUHRD18TB
BC3681305 AV639153
AJ473805 AV639153
BC36814950 GGCCS41TM
BZ559311 BAC61-60
BZ641457 OGCCS41TM
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BZ65111 PAC61-67
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Contact: Zeguang Han
Schineee National Human Genome Center at Shanghai
151 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
161: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Fax: 86-21-50801922
Fax: 86-21-50801922
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This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                    BI960110
CD432549
CNS010C9
CNS015VX
AU192776
AU193705
                                             BI996341
BI727879
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AL513886
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CC010084
CC405164
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EST.
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JOURNAL
COMMENT
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AUTHORS
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  AV755731 AV755731
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                                                                                                                                                     ; Search time 1443.21 Seconds (without alignments) 9447.586 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Minimum DB Maximum DB

Database

Result No.

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Searched:

EST 19-OCT-2000

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420 AATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGT 479
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Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
Clark,M., Johnson,S.L., Martin,J., Beck,C., Wylie,T., Underwood
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
X., Steptoe,M., Theising,B., Allen,M., Schurk,R., Ritter,E.,
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
                                                                                                                                                                            502 bp mRNA linear EST 13-FEB-2002 fm04e08.y1 Zebrafish adult retina cDNA Danio rerio cDNA clone IMAGE:4145367 5' similar to TR:Q9PWN4 Q9PWN4 RHODOPSIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watgon.wustl.edu
                               Length 502;
509 GCCACATAACGGGTC-ACCGTATGGCTTGGGATATGATGATGACTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Trace considered overall poor quality
Seq primer: T3 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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7.4%; Score 41.6; DE
Best Local Similarity 51.0%; Pred. No. 2.8;
Matches 98; Conservative 0; Mismatches
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/mol_type="mRNA"
/strain="wild-type"
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WashU Zebrafish EST Project 1998
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1 (bases 1 to 492)

10, "J. Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,Y., Li,Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z. Homo sapiens cDNA BM clones
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125 g 112 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                         /mol_type="mmRA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="BMPAKB01"
/tissue_type="Bone marrow"
/clone="type="Colone for the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the match of the 
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AV758366 BM Homo sapiens cDNA clone BMFAKA03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTAAT
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ilarity 72.5%; Pred. No. 0.013;
Conservative 0; Mismatches 29; Indels 1
                                                                                                                                                                                                                                                                                                                                                           Length 488;
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                                                                                                                                                                                                                                                                                                                                                                                                           24;
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Pred. No. 1e-05;
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/db_xref="taxon:9606"
/clone="BMFAKA03"
/tissue_type="Bone_marrow"
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                 l. .488
/organism="Homo sapiens"
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Best Local Similarity 77.9%;
Matches 88; Conservative (
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Homo sapiens
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Matches 79; Conserv
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AV758366/c
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402 bp mRNA linear EST 23-APR-2002 cDNA clone CM096g04_r 5', mRNA sequence.
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AV392165.1 GI:6546381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 GGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 GGCCGGCGCGCGCGCGAGTGGGAGGCCGCTACGCCGACGAGTCCGTGAGCTTGGGCGC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 TIGCICITICCTCTATCTICCTCTIGGCTTTGCTGTCTGTCTGACCGTTCCAGCTICCGC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 CCGCAAGGTGTTTGACGAGATCAAGGAGTACGTGCTGAACCTCAAGGCCCCAGAACCCCAG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 CTTCGCCGTCCGCTGCGTGGGCCACTCGCTGGGCGGCGGCACCGCCGGCTGCCTGTCGAT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydomonas reinhardtii
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="CM096g04_r"
/dev_stage="photoautotrophic growth"
/clone_lib="Chlamydomonas reinhardtii C9"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 CGACCTCGTGGGGTACATTCCGCTCGTCGGCGCCCCCTAGGGGGGGCGCTGCCAGGGCCCT
                                                                                                                                                                                                                                Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. al large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae,
Triticeae, Hordeum.
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/dev_stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. spontaneum top three leaves adult, heading
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Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Bmail: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
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/cultivar="H602"
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Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlawydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
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                                                                                                                                                                                                                     Contact: Charles Hauser
DCMB Box 91000
Duke University
                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: chauser@duke.edu
                                                                                                                                                                                                                                                                                                                      Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 circóccércédirederidadecarreteradadededededededededidecretedan 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yasukazu Nakamura

Contact: Yasukazu Nakamura

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

Location/Qualifiers
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/clone="CM083e05_r"
/clone="CM083e05_r"
/dev_stage="photoautotrophic growth"
/clone lib="Chlamydomonas reinhardtii C9"
/clone lib="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                     green
                                            Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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Lambda Zap II Chlamydomonas reinhardtii CDNA, mRNA sequence
B1996341
                                                                                                                                                                         Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. A large scale structural analysis of CDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags

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Pred. No. 5.1;
0; Mismatches 179; Indels
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/mol_type="mRNA"
/strain="C9"
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BX356664 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI015YB03 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.

88 c 93 g 398 t 506 others
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com Uhttp://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIOISCAO2NPI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 7.2%; Score 40.4; DB 13; 1 Similarity 10.4%; Pred. No. 7.1; 52; Conservative 233; Mismatches 212;
                                                                                                      347 caadaaddaaddaaddaadaadaaa 373
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/db_xref="taxon:9606"
/clone="CS0DI015YB03"
                                        GGAGAACACTCTTCCCGCTGCTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                              BX356664.1 GI:30378083
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                                                                                                                                                                                                                                                                                                                                                        Lefebvre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /olone_lib="C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCGCCGTCCGCTGCGTGGGCCACTCGCTGGCGGCGGCGCCCCGCCGGCTGCCTGTCGAT 286
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                                                                                                                                                                                                  Chlamydomonas reinhardtii
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 584).
Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebv,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGACCTCGTGGGGTACATTCCGCTCGTCGGCGCCCCCCTAGGGGGGCGCTGCCAGGGCCCTT
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       (normalized),
1031095C12.y1 C. reinhardtii CC-1690, Stress II (normalized)
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence
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/strain="CC-1690 wild type mt+ 21gr"
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Pred. No. 5.2;
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                                                                                                                                                                        Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Charles Hauser
DCMB Box 91000
Duke University
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                                                                                                      GI:15703574
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Tel: 919 613 8159
Fax: 919 613 8177
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/tissue type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6" ist strand cDNA was primed
/note="Vector: pCMVSPORT_6" ist strand cDNA was digested with Not I and cloned into
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
194 others
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AL513886
                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBA006ZGOBRP1&cluster=4924.f. Contact
cgi-bin/cluster.cgi?seq=CLOBA006ZGOBRP1&cluster=4924.f. Contact
Feng Liang Email : fliangelifetech.com VIR. :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA006ZGOBRP1.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Bmail: segref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed belongs to sequence cluster 4924.f
Invitrogen. This sequence belongs to sequence cluster 4924.f
                                                                                                                                                                                                                                                                                                                                                                                Enkaryotz Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12777380.
Contact: Genoscope
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                                863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BA006ZG08"
AL513886.2 GI:30463771
                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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G611605 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5485649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapba-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Cone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2016 row: n column: 18
High quality sequence stop: 567.
High quality sequence stop: 567.
                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 1162)
1 Math.MGC http://mgc.nci.nih.gov/.
National Indtitutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                    394 AGGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTCACC 453
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54.4%; Pred. No. 7.9;
iive 0; Mismatches 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                              : : | :: | :: | :: | 1095 SBTTSSTTTTTTSSSATBSB 1114
                                                                                                                                                                                                                                                                514 ATAACGGGTCACCGTATGGC 533
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 840)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser.C.M., Budiman, M.A., Bedall, J.A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 GGGCGCTGCCAGGCCCTGGCGCATGCCGTCCGGGTTCTGGAGGACGGCGTGAACTATG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol type="mRNA"
/cultivar="Chinese Spring"
/db xref="kaxon:6565"
/clone="whf25g19"
/tisne="whf25g19"
/tisne="whf25g19"
/dev_stage="spike at flowering date"
/dev_stage="peekes' scale 10.5.1"
/clone_lib="Y_Ogihara unpublished cDNA library, Wh_f"
a 107 c 110 g 77 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="ZMMEMA033124"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic_DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850,
                  Expressed genes in Triticum aestivum Unpublished Contact: Tadasu Shin-i Contex For Genetic Resource Information National Institute of Genetics 1111 Yata, Wabhima, Shizuoka 411-8540, Japan Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
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                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
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58.0%; Pred. No. 12;
tive 0; Mismatches
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/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db xref="taxon:4577"
                                                                                                                                                                                          Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence.
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CC335916.1 GI:30805329
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    Ogihara, Y. and Murai, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: TF
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Fax: 301-838-0208
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1 (bases 1 to 359)
Ogihara, Y. and Murai, K.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, Pooideae
7 Triticeae, Triticum.
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                         CCTGCGTTCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 CCTTACATGCGGCTTCGCCGACCTCGTGGGTACATTCCGCTCGTCGGCGCCCCCTAGG
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BJ252669.1 GI:20061830
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Pred. No. 12;
0; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
National Institute of Genetics
Tal: Nishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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/cultivar="Chinese Spring"
                                                                               392 CTAGGAACGCCAGCGTCCCCACCACGACA
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Triticum aestivum
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1 Similarity 58.0%;
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REFERENCE AUTHORS BASE COUNT

GSS 16-MAY-2003

USA

LOCUS DEFINITION

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EL01T0207B11.b Endosperm_4 Zea mays cDNA, mRNA sequence.
CD446071
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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| organism="Zea mays" |
| organism="Zea mays" |
| cult.ype="mm2n" |
| cultivar="W22" |
| db_xref="taxon:4577" |
| tisue type="Endosperm of 7-23DAP" |
| clone _ib="Endosperm 4" |
| clone _ib="vge="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="tayop="t
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Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E.
Messing,J.
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Pest Local Similarity 53.6%; Pred. No. 15;
Matches 81; Conservative 0; Mismatches 70; Indels
                                                                          Length 840;
                                                                          Query Match 7.0%; Score 39; DB 29; Length 84: Best Local Similarity 53.6%; Pred. No. 15; Matches 81; Conservative 0; Mismatches 70; Indels
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Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.
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Unpublished
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Search completed: December 20, 2003, 06:54:49 Job time : 1444.21 secs

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MOLECULE TYPE: cDNA HYPOTHETICAL: NO
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ANTI-SENSE: NO
FEATURE:
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Sequence 27, Appl
Sequence 27, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 13, Appl
Sequence 13, Appl
                                                            December 19, 2003, 18:11:23 ; Search time 40.4591 Seconds (without alignments) 6120.154 Million cell updates/sec
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                                                                                                                                Description
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Sequence 1
Sequence 4
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Sequence
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/cgn2_6/ptodata/2/ina/5B_COMB.seg:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seg:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seg:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-612-977-23
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US-08-927-597-27
US-08-927-597-27
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US-08-927-597-48
US-08-927-597-48
US-08-912-973-13
US-08-612-973-13
US-08-612-973-13
US-08-470-426B-14
                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                      569978 segs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                          OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Sequence 23, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MAREYNOFF, GUY
APPLICANT: BUYSE, MAREYNOFF, GUY
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR.1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNEY, THOWAS E.
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                           US-08-904-686A-9
US-09-315-850-9
US-08-314-616-3
US-08-304-616-3
US-08-315-850-3
US-09-315-850-3
US-08-384-616-11
US-08-384-616-11
                      30-204E-96
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1-08-904-686A-13
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COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 1487-10
TELECHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
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Best Local Similarity 100.
Matches 561; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
US-08-927-597-23
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Sequence 23, Application US/08927597
Sequence 23, Application:
APPLICANT: MAERTENS, GERT
APPLICANT: BORMAN, FONS
APPLICANT: BE MARTE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PURIFIED SOR DIAGNOSTIC AND THERAPEUTIC UNUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
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STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PATCH P.C.
OPERATING SYSTEM: P.C.DOS/WS-DOS
SOFTWARE: PATCH P.C.
SOFTWARE: PATCH P.C.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                                   Length 561;
                                                                                                             Indels
                                                                     100.0%; Score 561; DB 3; L
100.0%; Pred. No. 1.1e-141;
ive 0; Mismatches 0;
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                                                                                Query Match
Best Local Similarity 100.
Matches 561; Conservative
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US-08-927-597-23
                                          US-08-612-973-23
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                                    241 TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG 300
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241 TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG 300
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                                                                                                                                  301 GACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGC
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Patent No. 6245503

GENERAL INFORMATION:
APPLICANT: MARRYENS, GEERT
APPLICANT: DE MARRYNOFP, GUY
APPLICANT: DE MARRYNOFP, GUY
APPLICANT: DE WARTYNOFP, GUY
APPLICANT: DE WARTYNOFP, GUY
APPLICANT: DE WARTYNOFP, GUY
APPLICANT: DE WARTYNOFP, GUY
APPLICANT: DE WARTYNOFP, GUY
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 ATGATGATGAACTGGT 556
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                               Sequence 25, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
TITLE OF INVENTION: PURSE, MARIE-ANGE
TITLE OF INVENTION: PURSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111.
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COUNTRY: U.S.A.

ZIP: 22201-471.

ZIP: 22201-471.

ZIP: 22201-471.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATCORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 32,205
FREFERENCE/DOCKET NUMBER: 32,205

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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 556, Conservative
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; LOCATION: 1..600
US-08-612-973-25
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HYPOTHETICAL: NO
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LOCATION:
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ATGATGATGAACTGGT 556
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HYPOTHETICAL: NC
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/08612973
; Sequence 27, Application US/08612973
; Patent No. 6150134
; GENERAL INFORMATION:
    APPLICANT: MAERIENS, GEERT
    APPLICANT: BUSSN, FONS
    APPLICANT: BUSSN, MARIE-ANGE;
    APPLICANT: DE MARTYNOFF, GUY
    APPLICANT: DE MARTYNOFF, GUY
    APPLICANT: DE MARTYNOFF, GUY
    APPLICANT: DE MARTYNOFF, GUY
    APPLICANT: DE MARTYNOFF, GUY
    APPLICANT: DE MARTYNOFF, GUY
    APPLICANT: DE MARTYNOFF, GUY
    APPLICANT: DE MARTYNOFF, GUY
    TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
    INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
    INTERET: II.00 NORTH GLEBE ROAD
    CITY: ARLINGTON
    STATE: VIRGINIA
    COUNTRY: U.S.A.
    COUNTRY: U.S.A.
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
                                                                                                                                              1 ATGITGGGTAAGGGTCATCGATACCCTTACATGCGGCTTCGCCCGACCTCGTGGGGTACATT
                                                                                                                            1 AIGTIGGGIAAGGICATGGATACCCTTACAIGCGGCTTCGCCGACCTCGTGGGGTACAIT
                                                                                                      Gaps
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                                                                               Length 606;
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                                                                              99.1%; Score 556; DB 3; Le
100.0%; Pred. No. 2.5e-140;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 556; Conservative
                                    mat_peptide
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US-08-612-973-27
NAME/KEY:
LOCATION:
FEATURE:
                                   NAME/KEY:
LOCATION:
US-08-927-597-25
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFIERRATION THOMAS E: REGISTRATION NUMBER: 32,205
REFIERRATION NUMBER: 32,205
REFIERRATION NUMBER: 32,205
TELEPHONE: (703) 816-4000
INFORMATION FOR EQU ID NO: 27:
SEQUENCE CHARACTERISTICS:
LIENGTH: 636 base pairs
TELEFAX: (103) 816-4100
INFORMATION FOR EQU ID NO: 27:
SEQUENCE CHARACTERISTICS:
LIENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
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100.0%; Pred. No. 2.5e-140;
tive 0; Mismatches 0;
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Matches 556; Conservative
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Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: MARRTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARLTWOFF, GUY
APPLICANT: BUYSE, MARRTWOFF, GUY
APPLICANT: BUYSE, MARRTWOFF, GUY
APPLICANT: BUYSE, MARRTWOFF, GUY
APPLICANT: BUYSE, MARRTWOFF, GUY
APPLICANT: BUYSE, MARRTWOFF, GUY
APPLICANT: BUYSE, MARRTWOFF, GUY
APPLICANT: BUYSE, MARRTWOFF
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
CORRESPONDENCES 111
CORRESPONDENCES ADDRESS:
ADDRESSEE: 1100 NORTH GLEBE ROAD
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COMPUTE: Floppy disk
COMPUTE: Floppy disk
COMPUTE: DE Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACEARIEN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/Arm:-
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NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 ATGATGATGAACTGGT 556
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FOOR
APPLICANT: BOSMAN, FOOR
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PURIFIED FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 556; DB 3; Le
Pred. No. 2.5e-140;
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99.1%; Score 556; DB
Best Local Similarity 100.0%; Pred. No. 2.5
Matches 556; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDAER:
INTING DATE: 11-WAR-1966
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REFERENCE/DOCKET NUMBER: 1487-10
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMOTUNICATION INFORMATION:
TELECOMOTUNICATION INFORMATION:
TELECOMOTUNICATION INFORMATION:
TELECOMOTUNICATION INFORMATION:
TELECOMOTUNICATION INFORMATION:
TELECOMOTUNICATION INFORMATION:
TELECOMOTUNICATION INFORMATION:
TELECOMOTUNICATION:
SEQUENCE CHARACTERIFICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDENDESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                   Sequence 27, Application US/08927597 Patent No. 6245503
541 ATGATGATGAACTGGT 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
MOLECULE TYPE: O
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NAME/KEY:

LOCATION:

FEATURE:

NAME/KEY:

LOCATION:

LOCATION:

US-08-927-597-27
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Sequence 21, Application US/08927597

Sequence 21, Application US/08927597

GENERAL INPORMATION:

APPLICANT: BOSMAN, FONS

APPLICANT: BOSMAN, FONS

APPLICANT: BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE

TITLE OF INVENTION: POTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                       Length 723;
                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                         Score 556; DB 3; Le
Pred. No. 2.6e-140;
                                                                                                                                                                                                                              99.1%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSES: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
CONTRY: U.S.A.
ZIP: 22201-4714
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                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 556; Conservative
                                                                                                                                    mat_peptide
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| ANTI-SENSE: | FEATURE: | FEATURE: | LOCATION: | FEATURE: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCATION: | LOCAT
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            COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Ploppy MRS PC serior #1.0, Version #1.25 (BPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE: 11-MAR-1996
ATTORNEY AGENT INFORMATION:
NAME: BYRNE: THOWAS E.
REGISTRATION NUMBER: 32.205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE INCIDENCES: single
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100.0%; Pred. No. 2.6e-140;
tive 0; Mismatches 0;
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Matches 556; Conservative
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COMPUTER READABLE FORM:
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MOLECULE TYPE: CI
HYPOTHETICAL: NO
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FEATURE:
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, LOCATION:
US-08-927-597-21
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                                                                                                  181 CTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAAACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08927597
Patent No. 6745503
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SERVE
APPLICANT:
BOSMAN, FONS
APPLICANT:
BUYSE, MARTYNOFF
TITLE OF INVENTION:
PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION:
PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZU210-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION UNMBER: US/08/927,597
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 529 ATGGCTTGGGATATGATGATGAACTGGT 556
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APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
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                                                                                                                                                                                                                                                                   APPLICANT: MARRIENS, GEERT APPLICANT: BOSMAN, PONS
APPLICANT: BOSMAN, PONS
APPLICANT: BE MARTYNOFF, APPLICANT: BE WARTYNOFF, APPLICANT: BE WARTYNOFF, APPLICANT: BIYSE, MARTIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, TROWAS E.
REFERENCE/DOCKET NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Pred. No. 2.8e-118;
0; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: PID PC
COMPUTER: TEN PC
COMPUTER: TEN PC
COMPUTER: PS PC
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   RESULT 9
US-08-612-973-5
; Sequence 5, Application US/08612973
; Patent No. 6150134
; GENERAL INFORMATION:
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                                                                   541 ATGATGATGAACTGGT
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 88.5
Matches 556; Conservative
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; LOCATION: 1..789
US-08-612-973-5
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LOCATION:
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APPLICANT: BOSMAN, FONS.
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYER, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES:
ADDRESSE: 1110
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72;
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Pred. No. 2.4e-117;
0; Mismatches 0; Indels 7;
                                                                                                                                                                                                                                                                                               COMPUTER NOTES FIOPPY GISK
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PLONGS/MS-DOS
SOFTWARE: PACATION NE-BESS #1.0, Version #1.25 (EPO)
SOFTWARE: PACATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOWAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 1487-10
TELECHONE: (703) 816-4100
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TELECHON
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Best Local Similarity 88.5%;
Matches 553; Conservative
                                                                                                                                                                                STREET: 1100 NORTH GLEBE RCITY: ARLINGTON
STATE: VIRGINIA-
COUNTRY: U.S.A.
ZIP: 222014714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-612-973-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 IGCIGGGIAGCGCTCACCCCCACGCTAGGAACGCCAGCGTCCCCAACGACA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTTGGCTTTGCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       72;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 474; DB 3; Length 795;
Pred. No. 2.8e-118;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGCTTGGGATATGATGAACTGGT 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.5%;
88.5%;
                           TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                               NAME/KEY: mat_peptide;
LOCATION: 1..789
US-08-927-597-5
                                                                                                                                                                                                                                                                                      1..792
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                              MOLECULE TYPE: CHYPOTHETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . . . . . .
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                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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Best Local Simil
Matches 556; C
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Sequence 47, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: MAERIENS, GEERT

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183 183 243 243

363 363 423 438

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64 CTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGGC 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                184 TIGGCTITIGCTGTCCTGTCTGACCGTTCCAGCTTATGAAGTGCGCAACGTGTCC
                                                                                                                                                                                                        4 TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATTCCG
                                                                                                                                                                                                                                            64 CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484 GACCTCTGCGGATCTGTCTTCCTCGTCCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 GAGACGCTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG
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                                                                                                                                                              4 TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGGTACATTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 49, Application US/08612973

Sequence 49, Application US/08612973

GENERAL INFORMATION

APPLICANT: MAERTENS, GERT

APPLICANT: BOSMAN, FONS

APPLICANT: BUYSE, MARIE-ANGE

TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

CORRESPONDENCE ADDRESS:

ADDRESSE:

ADDRESSE:

STREET: 1100 NORTH GLEBE ROAD
                                                                                                                        72;
                                                                              Length 2082;
                                                                                                                      Indels
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                                                                          Score 471; DB 3; 1
Pred. No. 2.4e-117;
0; Mismatches 0;
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                                                                                84.0%;
88.5%;
                                                                          Query Match
Best Local Similarity 88.5
Matches 553; Conservative
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
; NAME/KEY:
; LOCATION:
US-08-927-597-47
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                                        364 TGGGTAGCGCTCACCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACATA 423
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                                                                                                                                                                                                                                                             472 GAGACGGTGCAGGACTGCAATTGCTCAATCCTATCCCGGCCACATAACGGGTCACGTATG
                                                                                                                                                                             Sequence 47, Application US/08927597
Patent No. 6245503
GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Date PC-DOS/MS-DOS
SOFRWARE: PatentIn Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
PILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS: 2.205
REFISTRATION NUMBER: 32,205
REFISCHMONICATION INFORMATION:
TELEFRONE: (703) 816-4100
INFORMATION FOR ESQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2082 base pairs
TELEGTH: 2082 base pairs
                                                                                                                                                                                                                                                                                                                                            532 GCTTGGGATATGATGATGAACTGGT 556
                                                                                                                                                                                                                                                                                                                                                                                    604 GCTTGGGATATGATGATGAACTGGT 628
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ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                             424 CGACGCCACGTCGAT-----
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: VIRGINIA COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
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NAME/KEY:
LOCATION:
FEATURE:
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US-08-927-597-47
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64 CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG 123
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                                                                                                                                                                            US=UB=927-59/-49

Sequence 49, Application US/08927597

Fatent No. 6245503

Patent No. 6245503

Patent No. 6245503

APPLICANT: MARRITENS, GERRT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
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APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: PALLICANTON: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESSS:
ADDRESSEB: NIKON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
STREET: 1100 NORTH GLEBE ROAD
APPLICATION
STATE: VIRGINIA
COMPUTER READABLE FORM
MEDIUM TYPE: FLORPY disk
COMPUTER READABLE FORM
MEDIUM TYPE: PLORPY disk
COMPUTER PATENTING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/927,597
BAPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72;
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Best Local Similarity 88.5%; Pred. No. 2.5e-117;
Matches 553; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE:
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 1487-10
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
'ENGTH: 2433 base pairs
                                                                532 GCTTGGGATATGATGATGAACTGGT 556
                                                                                      955 GCTTGGGATATGATGATGAACTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
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LOCATION:
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LOCATION:
US-08-927-597-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.0%; Score 471; DB 3; Length 2433; 88.5%; Pred. No. 2.5e-117; rive 0; Indels 7;
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION WHERE: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
CLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 1487-10
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR ESQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2433 base pairs
LENGTH: 2433 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: TOPOLOGY: linear

"AVER: TYPE: CDNA
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553; Conservative
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ANTI-SENSE: NO
FEATURE:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
US-08-612-973-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Si
Matches 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          715
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241 TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTGTATGAGGCAGCG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.2%; Score 461.4; DB 3; Best Local Similarity 86.9%; Pred. No. 6.4e-115; Matches 550; Conservative 0; Mismatches 11;
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TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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   CTCGTCGGCCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG 474
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                                                                                                     TTGGCTTTTGCTGTCCTGTCCGGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC
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                                                                  595 GGGATGTACCATGTCACGACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
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APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUMTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILLING DATE: 11-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTTGGGATATGATGATGAACTGGT 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/ACENT INFORMATION:
NAME: BYRNE, THOMAS B.
REGISTRATION NUMBER: 32,205
REGISTROF/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/08612973
; Patent No. 6150134
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US-08-612-973-7
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GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: December 19, 2003, 16:55:48; Search time 2294.49 Seconds
(without alignments)
10804.703 Million cell updates/sec
Title:
US-09-899-303A-25
Perfect score: 606
Sequence:
1 ATGTTGGGTAAGGTCATCGA.....TGCTCCGGATCCTCTAATAG 606
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Total number of hits satisfying chosen parameters: 5777422

2888711 seqs, 20454813386 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : GenEmbl:*

1: gb ba:*
2: gb_htg:*
3: gb_nn:*
5: gb_on:*
6: gb_ph:*
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10: gb_pi:*
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Pred. No. is the number of results predicted by chance to have a

em_htgo_hum:* em_htgo_mus:* em_htgo_other:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Score | atc | Ä ; | DB | ۱ ۵ | cription |
|-----------------------|-------|------------|----------|--------------------|---------------------|
| 909 | 100.0 | 606 606 | 99 | A48687 AR157338 | nce |
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| ú | ٠, | 3296 | 14 | AB008447 | AB008447 Hepatitis |

ALIGNMENTS

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| • | | Sequence 25 from Patent WO9604385 | | A48687.1 GI:2302400 | | ied | ied | unclassified. | 1 (bases 1 to 606) | : | HEP! | THERAPEUTIC USE | Patent: WO 9604385-A 25 15-FEB-1996; |
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    .603
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INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.
Location/Qualifiers
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Matches 606; Conservative 0; Mismatches 0; Indels
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Patent: US 6245503-A 25 12-JUN-2001;
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Purified Hepatitis C Virus envelope proteins therapeutic use
Patent: WO 02055548-A 25 18-JUL-2002;
INNOCENETICS N.V. (BE)
Location/Qualifiers
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Sequence 25 from Patent WO02055548.
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Hepatitis C virus
Viruses; ssRNA positive-strand
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QDCNCSIYPGHITGHRMAWDMMANWSPTTALVVSQLLRIL"
                              Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Mertens,G., Bosman,F., de Martynoff,G. and Buyse,M.A.
Recombinant vectors for producing hcv envelope proteins
Patent: EP 1211315-A 25 05-JUN-2002;
Innogenetics N.V. (BE)
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| Oy 421 ATACGACGCCACGTCGATTCCCAGCTGTCACCATCTCGCCTGCCGGCATGAGACGGTG 480 | A48683 LOCUS A48683 A48683 A48683 ACESSION ACRESSION A48683 VERSION A48683 Unidentified ORGANISM Unidentified ORGANISM Unidentified AUTHORS AU | | ss at_peptide ounr 126 | Owigin Query Match Query Match Query Match Query Match Best Local Similarity 99.5%; Pred. No. 6.8e-122; Best Local Similarity 99.5%; Pred. No. 6.8e-122; Back Local Similarity 99.5%; Pred. No. 6.8e-122; Back Local Similarity 99.5%; Pred. No. 6.8e-122; Matches 600; Conservative 0; Mismatches 3; Indels 0; Gaps 0; A TGTTGGGTAAGGTCATCGATACCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT 60 Db 1 ATGTTGGGTAAGGTCATCGATACCTTACATGCGGCTTCGCCGATCGGGTACATT 60 Oy 61 CCGCTCGTCGGCGCCCCCTAGGGGGCTGCCAGGGCCTTGCGCATGGCTTTCTCTATCTT 120 Oy 121 CTGGAGGACGGCTGAACTATGCAACAGGGCCTGGCGGTTGCTCTTTCTCTATCTTC 180 Db 121 CTGGAGGACGGCTGAACTATGCAACAGGGAATTTGCCGGGTTGCTCTTTCTT |

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420 480

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Purified Hepatitis C Virus envelope proteins for diagnostic
therapeuto use
Patent: WO 02055548-A 21 18-JUL-2002;
INNOGENETICS N.V. (BE)
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Sequence 21 from Patent WO02055548.
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/db_xref="taxon:11103"
/note="unnamed protein product"
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Pred. No. 6.8e-122;
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Sequence 21 from Patent
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VNYATGNLPGCVPCVRENNSSRCWVALTPTLAARNASVPTTTIRRHVDSQLFTISPRRHETV
ODCNCSIYPGHITGHRWAWDNWMWNWSPTTALVVSQLLRIVIEGRHHHHHH"
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Sequence 27 from patent US 6245503.
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/note="unnamed protein pro/codon_start=1
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Pred. No. 6.8e-122;
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Patent: WO 9604385-A 27 15-FEB-1996;
INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.
Location/Qualifiers
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Sequence 27 from Patent WO9604385.
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A48689.1 GI:2302402
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/note="unnamed protein product"
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QDCNCSIYPGHITGHRWAWDWMGNWSPTTALVVSQLLRIVIEGRHHHHHH"
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27 from Patent WO02055548.
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/organism="Hepatitis C vi/organism="genomic DNA"
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic
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Pred. No. 1e-121;
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Patent: US 6245503-A 27 12-JUN-2001;
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                    Maertens.G., Bosman,F. and Buyse,M.A.
Purified Hepatitis C Virus envelope proteins for diagnostic and
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Pred. No. 1e-121;
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Patent: WO 02055548-A 27 18-JUL-2002;
INNOGENETICS N.V. (BE)
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unidentified
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1 (Dases 1 to 561)
Maertens, G., Bosman, F., De, M.G. and Buyse, M.
Maertens, G., Bosman, F., De, M.G. and Buyse, M.
THERAPEUTIC USB
PATENT: WO 9604385-A 23 15-FEB-1996;
INDOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.
Location, Qualifiers cretragecrimacionerecrareceaerrecaecriceaerrareaagraceaaecare TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGGG 101 GACATGATGATGACCCCGGGTGCGTGCCTGCGTTCGGGAGAAACAACTCTTCCGGC ccecrcarcacccccraagaaccccraccaaaaccccraacccaraaccarcaacarc crigaladalcidaladaladaladaladagalatatacccagatactictitatatata 1 AIGTIGGIAAGGICAICGAIACCCTIACAIGCGGCTICGCCGACCTCGIGGGGIACAIT Gaps . 0 Length 561; 0; Indels 91.7%; Score 556; DB 6; Le ilarity 100.0%; Pred. No. 1.4e-112; Conservative 0; Mismatches 0; 481 ð

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ODGNCSIYPGHITGHRMAWDWMMW"
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                                                                                                                                                                                                    Maertens,G., Bosman,F., de Martynoff,G. and Buyse,M.A.
Recombinant vectors for producing hov envelope proteins
Patent: EP 1211315-A 23 05-JUN-2002;
Innogenetics N.V. (BE)
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11 Similarity 100.0%; Pred. No. 1.4e-112;
556; Conservative 0; Mismatches 0;
                                                                                                                    Hepatitis C virus
Hepatitis C virus
Viruses; seRNA positive-strand viruses,
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1. 558
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Sequence 23 from Patent EP1211315.
AX452772
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/organism="Hepatitis C
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RESULT 15
AX452772
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                                                                                                                                                                                                                                                                                         Unclassified.
1 (bases 1 to 561)
Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
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| 13 513.2 84.7 243 17 AAL19914 Hepatitis C VI | | 13.2 | 84.7 | 2086 | 11 | AAT12973 | El const |
| 14 50.2. 8.19 | | 13.2 | | 2433 | 17 | AAT12974 | E1 CO |
| 15 456.4 75.3 643 17 AAL12706 HGV B1 CONSIGNA 16 456.4 75.3 643 17 AAL48915 HGPARILIS CONFICUA 17 453 74.8 673 19 AAA48305 HGV Core profect 18 452.4 74.7 2540 14 AAA48305 HGV Core profect 20 452.4 74.7 2540 15 AAA63753 HGPARILIS C VI 21 452.4 74.7 2540 15 AAA63753 HGPARILIS C VI 22 452.4 74.7 2540 15 AAA63753 HGPARILIS C VI 23 452.4 74.7 9605 24 ABK91428 HGPARILIS C VI 24 452.4 74.7 9605 24 ABK91428 HGPARILIS C VI 25 452.4 74.7 9605 24 ABK91428 HGPARILIS C VI 26 452.4 74.7 9605 24 ABK91428 HGPARILIS C VI 27 452.4 74.7 9605 24 ABK91439 HGPARILIS C VI 28 452.4 74.7 9605 24 ABK91431 HGPARILIS C VI 29 452.4 74.7 9605 24 ABK91431 HGPARILIS C VI 29 452.4 74.7 9605 24 ABK91431 HGPARILIS C VI 29 452.4 74.7 9605 24 ABK91431 HGPARILIS C VI 29 452.4 74.7 9605 24 ABK91431 HGPARILIS C VI 29 452.4 74.7 9605 24 ABK91431 HGPARILIS C VI 29 452.4 74.7 9605 24 ABK91431 HGPARILIS C VI 29 452.4 74.7 9605 24 ABK91431 HGPARILIS C VI 20 452.4 74.7 1106 21 AAA98965 HGV BL CONSERUAL 20 452.4 74.7 1106 21 AAA98965 HGV BL CONSERUAL 21 450.8 74.4 1880 13 AAA06673 HGPARILIS C VI 20 450.8 74.4 1880 13 AAA06673 HGPARILIS C VI 20 450.8 74.4 1880 13 AAA06673 HGPARILIS C VI 20 450.8 74.1 3461 15 AAA066063 HGV BL CONSERUAL 21 449.2 74.1 3461 16 AAT30386 S VUTR/CORE/ENV 22 458P-1996 (first entry) 24-SEP-1996 (first entry) 24-SEP-1996 (first entry) 24-SEP-1996 (first entry) | | 02.2 | | 2434 | 24 | AAL48940 | Hepatitis C virus |
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| 21 452.4 74.7 9605 24 ABK91411 Hepatitis C vi | | | | 2540 | 12 | AAQ63753 | NANBHV genomic fr |
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HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera; Maertens G Bosman F, Buyse M, De Martynoff G, 94EP-0870132 95WO-EP03031 (INNO-) INNOGENETICS NV Hepatitis C virus 29-JUL-1994; 31-JUL-1995; WO9604385-A2 15-FEB-1996

Purifying recombinant hepatitis C virus (HCV) El and E2 envelope

NPI; 1996-129401/13

TAATAG 606

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AATI2704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins.

C in vectors for the production of recombinant E1, E2, and E1/E2 proteins.

C in the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a crarying out a sample, and in a serotyping assay for detecting one or antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated control of HCV. The new purification method presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and climinates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known
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proteins - in presence of di.sulphide bond cleavage agent, to
produce proteins suitable for direct use in vaccines or diagnostic
assays of HCV
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV) -specific antibodies, comprising a inducing hepatitis C virus (HCV) -specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and specific oligomeric recombinant envelope proteins aclected from an B1 and useful for inducing HCV-specific antibodies or for immunising humans useful for inducing HCV-specific antibodies or for immunising humans vaccines or therapeutics, in HCV B1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                   New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
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0
                                                                                                                                Hepatitis C virus; HCV; El protein; E2 protein; infection; gene; virucide; immunostimulant; vaccine; ds.
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Pred. No. 1.2e-152;
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                                                                                                    Hepatitis C virus clone HCCI39 B1 protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 606 BP; 109 A; 193 C; 167 G; 137 T; 0 other;
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ilarity 100.0%; Pred. No. 1.2
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 177-178; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Buyse M;
                      BP.
                                                                                                                                                                                                                                                                                              11-JAN-2001; 2001US-260699P.
30-AUG-2001; 2001US-315768P.
                                                                                                                                                                                                                                                                   11-JAN-2002; 2002WO-EP00219.
                        DNA; 606
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                            (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                                                                                                         Bosman F,
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                                                                                                                                                                                                                                                                                                                                                                                                     2002-599657/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from HCV infection
                        AAL48927 standard;
                                                                                                                                                                                  Hepatitis C virus.
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                                                                                                                                                                                                               WO200255548-A2.
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invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed El. E2 and El/E2, and eliminates contaminating proteins. Antigens isolated using this method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCCGGTTGCTCTTTCTCTATCTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 GACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 IGCIGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACCACACA
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                                                                                                                                                                                                                                                                                                                                                                                         DB 17; Length 723;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                  Score 598.2; DB 17
Pred. No. 1.6e-150;
0; Mismatches 3;
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Best Local Similarity 99.5%;
Matches 600; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT
                                                                                             241 TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
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agent, to
or diagnostic
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                                        gene;
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Best Local Similarity 99.5%; Pred. No. 1.6e-150;
Matches 600; Conservative 0; Mismatches 3; Indels 0;
                                 Hepatitis C virus; HCV; El protein; E2 protein; infection; virucide; immunostimulant; vaccine; ds.
      Hepatitis C virus clone HCCI37 El protein coding sequence.
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                                                                                                                                                                                                                                                                                      Buyse M;
                                                                                                                                                                                                            11-JAN-2001; 2001US-260699P.
30-AUG-2001; 2001US-315768P.
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                                                                                                                                                                                                                                                         (INNO-) INNOGENETICS NV.
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                                                                                      Hepatitis C virus.
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AATI2704-TI2709 and AATI2961-TI2974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins.

C in vectors for the production of recombinant E1, E2, and E1/E2 proteins.

C in vectors for the production of recombinant hod of the invention. In the method, the envelope proteins are purified by a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage agent, after lysis of recombinant host cells.

C for constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a scrotyping assay for detecting one or antibodies types of HCV present in a biological sample.

C constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the 540 900 480 480 420 420 HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera; 541 ATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTGCGGATCCTC CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT TGCTGGGTAGCGCTCACCCCCACGCAGCTAGGAACGCCAGCGTCCCCACCACGACA ATACGACGCCACGTCGATTCCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTG Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV Maertens G; De Martynoff G, Claim 23; Fig 21; 146pp; English. BP. 95WO-EP03031. 94EP-0870132. AAT12964 standard; DNA; 636 (first entry) (INNO-) INNOGENETICS NV. HCV El construct HCCI40. Bosman F, Buyse M, WPI; 1996-129401/13. Hepatitis C virus. 601 TAA 603 CAA 603 31-JUL-1995; 29-JUL-1994; WO9604385-A2 24-SEP-1996 15-FEB-1996. AAT12964; 421 421 481 601 361 RESULT 5 g ð g ò 셤 ò à g

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                                                                                                                        Gaps
conformation of the recombinantly expressed El, E2 and El/E2, and eliminates contaminating proteins. Antigens isolated using this rare more reactive with human sera than those isolated by known
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                                                                   Sequence 636 BP; 119 A; 203 C; 174 G; 140 T; 0 other;
                                                                                           Score 597.4; DB 17
Pred. No. 2.4e-150;
0; Mismatches 1;
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligometric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or B2 proteins are useful as vaccines or therapeutica, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present
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Pred. No. 2.4e-150;
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Best Local Similarity 99.8%;
Matches 598; Conservative
11-JAN-2001; 2001US-260699P.
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                                                   (INNO-) INNOGENETICS
                                                                                    Bosman
                                                                                                                  WPI; 2002-599657/64.
P-PSDB; AAO18669.
                                                                                                                                                                                                                       from HCV infection
                                                                                  Maertens G,
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The present invention relates to new therapeutic vaccine compositions for
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                                                                                                                                                                                                                                                                                                                                                        ATACGACGCCACGTCGATTCCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTG
                                                                                                                                                                                                                                                                                                                                                                                                    CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT
 CTGGAGGACGCCTGAACTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTC
                      TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
                                                                                                                                                            241 TCCGGGATGTACCATGTCACGAACGACTACTCCAACCTCAAGCATTGTGTATGAGCCAGCG
                                                                                                                                                                                                 GACATGATICA,TGCACACCCCCGGGGTGCGTGCCCTTGCGGGAGAAACAACTCTTCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus clone HCCI38 El protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 175-176; 243pp; English.
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30-AUG-2001; 2001US-315768P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maertens G, Bosman F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-599657/64.
P-PSDB; AAO18667.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMTI2704-TI2709 and AATI2961-TI2974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins of the production of recombinant proteins are then be isolated using a method of the carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage agent, after 1/sis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used to vaccinating humans against HCV, for in vitro detecting one or antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated the agencype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and conformation of the recombinantly expressed E1, E2 and E1/E2, and conformation energy in the presence is a more reactive with human sera than those isolated by known
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                                                                                                                                                                                                                                  HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
CCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT
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                                                                                                           AAT12962 standard; DNA; 561 BP
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                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
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Maertens

De Martynoff G,

(INNO-) INNOGENETICS NV
Bosman F, Buyse M, De
WPI; 1996-129401/13.

95WO-EP03031.

Hepatitis C virus. WO9604385-A2. 15-FEB-1996.

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inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or E2 proteins are useful as vecines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence
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                                                                                                                                                                                                                                     is a coding sequence described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                   Sequence 561 BP; 103 A; 176 C; 155 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                               Score 556; DB 24; L
Pred. No. 2.9e-139;
                                                                                                                                                                                                                                                                                                                            Query Match
91.7%; Score 556; DB
Best Local Similarity 100.0%; Pred. No. 2.9
Matches 556; Conservative 0; Mismatches
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and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a canstructs containing the purified HVV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known
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Purifying recombinant hepatitis C virus (HCV) E1 and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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                                                                                                                                                                                      Claim 23; Fig 21; 146pp; English.
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Best Local Similarity 88.9%;
Matches 600; Conservative
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        New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
                                                                                          ATGCCTTGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTG
                                                                                                                      CATGAGACGGTGCAGGAGTGCAATTGGTCAATCTATCCCGGCCACATAACGGGTCACGT
                                                                              -----TCCCAGCTGTTCACCATCTCGCCGG
                                                       Hepatitis C virus; HCV; El protein; El protein; infection; gene; virucide; immunostimulant; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus clone HCCI10A B1 protein coding sequence.
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30-AUG-2001; 2001US-315768P.
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                                                                                                                                                                                                           CICCGGATCCTCTAA 603
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P-PSDB; AAO18661.
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                                         72;
                     DB 24; Length 795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus E2 protein related coding sequence SEQ
                                         Indels
Sequence 795 BP; 130 A; 240 C; 231 G; 194 T; 0 other;
                     Score 516.2; DB 24;
Pred. No. 1.5e-128;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                   421 ATACGACGCCACGTCGAT-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; B1 protein; virucide; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               crccegarcccacaa 675
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                       ch 85.2%; al Similarity 88.9%; 600; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus.
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                            Query Match
                                        Local
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1
and E2 protein coding sequence constructs. These sequences are included
the vectors for the production of recombinant E1, E2, and E1/E2 proteins.
The recombinant proteins can then be isolated using a method of the
invention. In the method, the envelope proteins are purified by
carrying out a disulphide bond cleavage for a reduction step with a
disulphide bond cleavage agent, after lysis of recombinant host cells.
The constructs containing the purified HCV envelope proteins can be used
for vaccinating humans against HCV, for in vitro detection of HCV
continues serological types of HCV present in a biological sample. The
constructs can also be immobilised on a solid substrate and incorporated
into a reversed phase hybridisation assay for determining the presence or
the genotype of HCV. The new purification method preserves the
conformation of the recombinantly expressed E1, E2 and E1/E2, and
eliminates contaminating proteins. Antigens isolated using this method
conformation with human sera than those isolated by known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Fig 21; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT12973 standard; DNA; 2086 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-EP03031.
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                                                                                                                                                                                                                                                                                                  592 CGGATCCTCTAA 603
                                                                                                                                                                                                                                                                                                                                                   675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HCV El construct HCCI65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                 664 CGGATCCCACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buyse M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an E1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 GAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTC 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGGTAAGGTCATCGATACCCTTACATGCGGGCTTCGCCGACCTCGTGGGGTACATTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGCTTTGCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
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                                                                                                                                                                                                                                                                                                                                                                     New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGGTACATTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 513.2; DB 24; Length 2082; Pred. No. 1.3e-127; 0; Mismatches 3; Indels 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of patients suffering from HCV infection. The is a coding sequence described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 2082 BP; 366 A; 634 C; 600 G; 482 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGACGCCACGTCGAT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 206-209; 243pp; English
                                                                                                                                                                                                                                                 Buyse M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.7%;
                                                                        11-JAN-2002; 2002WO-EP00219.
                                                                                                                    11-JAN-2001; 2001US-260699P. 30-AUG-2001; 2001US-315768P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 597; Conservative
                                                                                                                                                                                             (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                              Bosman F,
                                                                                                                                                                                                                                                                                          WPI; 2002-599657/64.
P-PSDB; AAO18678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              From HCV infection
                                                                                                                                                                                                                                              Maertens G,
                       18-JUL-2002
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Best Local S
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                                                                                                                                                                                                                                                    604 GCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
TCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT
                                            544 dadacedriccaecriccaarriccreaarcratecreecceccaraaacegercaccerare
                                                                                                                                                                                                                      532 GCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ig recombinant hepatitis C virus (HCV) B1 and B2 envelope s - in presence of dissulphide bond cleavage agent, to proteins suitable for direct use in vaccines or diagnostic
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1 and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins.

C in vectors for the production of recombinant E1, E2, and E1/E2 proteins.

CC invention. In the method, the envelope proteins are purified by invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or antibodies in a sample and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated containing the presence or into a reversed phase hybridisation assay for determining the presence or into a reversed phase hybridisation assay for determining the presence or into a reversed phase hybridisation assay for determining the presence of into a reversed phase hybridisation assay for determining the presence of into a reversed phase hybridisation assay for determining the presence of into a reversed phase hybridisation assay for determining the presence of into a reversed phase hybridisation assay for determining the presence of into a reversed phase hybridisation assay for determining the presence of into a reversed phase hybridisation assay for determining the presence of into a reverse presence of the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and e1/E2, and enverse presence of the more reactive with human sera than those isolated using this method creating the presence of the conformation of the revombinance of the preserves the more more reactive with hum
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Pred. No. 1.3e-127;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2433 BP; 434 A; 745 C; 714 G; 540 T; 0 other;
                                                                                                                                                                                            Maertens G;
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                                                                                                                                                                                              De Martynoff
                                                                                                                                                                                                                                                                                                                                                                                                                           claim 23; Fig 21; 146pp; English.
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Best Local Similarity 88.8%;
Matches 597; Conservative (
                                                                                              94EP-0870132
                                                95WO-EP03031
                                                                                                                                                 (INNO-) INNOGENETICS NV
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                                                                                                      29-JUL-1994;
                                                   31-JUL-1995;
15-FEB-1996
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                                                                                                                Gaps
                                                                                                                72;
                                                             DB 17; Length 2086;
                                                                                                                   Indels
                BP; 366 A; 635 C; 601 G; 484 T; 0 other;
                                                                Score 513.2; DB 17
Pred. No. 1.3e-127;
0; Mismatches 3;
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   DB 24; Length 2434;
                                                                    Indels
                              Pred. No. 1.2e-124;
0; Mismatches 3;
      Score 502.2;
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                                                                                                                                         835 GACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCGGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus E2 protein related coding sequence SEQ ID NO: 49.
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438 834 470 894 530

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AMIL2704-T12709 and AMIL2961-T12974 represent hepatitis C virus (HCV) El cand E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant El, E2, and El/E2 proteins. C in vectors for the production of recombinant El, E2, and El/E2 proteins. C invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage agent, after 1945 of recombinant host cells. C disulphide bond cleavage agent, after 1945 of recombinant host cells. C antibodies in a sample, and in a servityping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed El, E2 and El/E2, and eliminates contaminating proteins. Antigens isolated using this method are mere reactive with human sera than those isolated by known
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                                                                                                                                                                                                                                                                                  Purifying recombinant hepatitis C virus (HCV) E1 and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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Best Local Similarity 86.8%; Pred. No. 1.5e-112;
Matches 545; Conservative 0; Mismatches 11; Indels 72;
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                                                                                                                                                                         De Martynoff G, Maertens G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 23; Fig 21; 146pp; English.
95WO-EP03031
                                                       94EP-0870132
                                                                                                                     (INNO-) INNOGENETICS NV
                                                                                                                                                                                   Buyse M,
                                                                                                                                                                                                                                              WPI; 1996-129401/13
                                                                 29-JUL-1994;
   31-JUL-1995;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 488)
6 (b. J. Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H., Gu, Y., Li, N., Qian, B., Liu, P., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gao, G., Wang, Z., Zhang, Q., Chen, S., Han, Z. and Chen, Z. Unpublished
AV392783 AV392785
BV392165 AV392165
B1727879 1031037A0
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B1727879 1031095C1
BW318259 AGENCOURT
AL513886 AL513886
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BV246716 BV246716
CC335916 OGUMAGOTV
CD446071 EL01T0207
AL053013 Drosophil
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AL098787 Drosophil
AL195775 Drosophil
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CC401084 PUGAJ92TB
CC405164 PUFFDIRTD
CC359028 PUHFDIRTD
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BZ555011 pacg1-60
BE499055 WHE0364_A
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Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
151 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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BE490055
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JOURNAL
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AV758366 AV758366
BI879124 fm04e08.y
AV835132 AV835132
                                                                                                  2003, 18:03:34 ; Search time 1558.97 Seconds (without alignments) 9447.586 Million cell updates/sec
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                GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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                               Copyright
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Minimum DB R Maximum DB R

Database

Result Š

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Searched:

EST 19-OCT-2000

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Email: zbraiksh@watson.wustl.edu
Email: zbraiksh@watson.wustl.edu
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germany
distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germany
fiveb considered overall poor quality
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; Cyprinidae; Danio.
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; Cyprinidae; Danio.
; Lidses I to 502)
; Clark, M. Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy S., Hillier, L., Kucaba, T., Martin, J., Bowers, Y., Person, B., K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
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                                                                                                                                              502 bp mRNA linear EST 13-FEB-2
fm04e08.yl Zebrafish adult retina cDNA Danio rerio cDNA clone
IMAGE:4145367 5' similar to TR:Q9PWN4 Q9PWN4 RHODOPSIN. ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
6.9%; Score 41.6; DB 12; Length 502;
Best Local Similarity 51.0%; Pred. No. 2.8;
Matches 98; Conservative 0; Mismarches 94; Indels 0
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mol type="mRNA"
strain="wild-type"
/db xref="taxon:7955"
/clone="IMAGE:4145367"
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Danio rerio
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                                                                                                                                                                                                                                          568 GCCCTGGTGGTATCGCA 584
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 CIGITCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTAT 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
Contact: Equang Han
Contact: Equang Han
Contact: Sequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
128 c 125 g 112 t 3 others
                                                                                                                                              /tissue type="Bone marrow"
/cell type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM35.8"
/clone_lib="BM"
/clone="Vector: pTriplEx2, Site_1: sfilA; Site_2: sfilB"
/note="Vector: pTriplEx2, Site_1" 4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV758366 AV Homo sapiens cDNA clone BMFAKA03 5', mRNA sequence
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Pred. No. 0.0012;
0; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                    Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                38; Indels
                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.3%; Score 68.2; DB 9;
Best Local Similarity 72.3%; Pred. No. 3.6e-07;
Matches 102; Conservative 0; Mismatches 38;
                                            organism="Homo sapiens"
                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564 AACGGCCCTGGTGGTATCGCA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 cecrecrarearcarecera 263
                                                                                                                            /clone="BMFAKB03"
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Best Local Similarity 67.2%;
Matches 92; Conservative 0
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402 bp mRNA linear EST 23-APR-2002 AV392783 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii AV392783 AV392783
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 CCGCAAGGTGTTTGACGAGATCAAGGAGTACGTGCTGAACCTCCAAGGCCCAGAACCCCAG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 GGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 GéccGGCGCGCGCGAGTGGGAGGCCGCTACGCGCACGACTCCGTGAGCTTGGGCGC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3055"
/clone="CW096g04_r"
/dev_stage="phototrophic growth"
/clone_lib="hidpaydomonas reinhardtii C9"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                         Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 chrceccencecreceneeecacrecreeececececaccecececrecrerer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 402)
Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. A large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                        531
                                                          181 ACCGNÁCTCGCCTCCCTCTCCGCCCCCAGCGCACCACGAACG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 179; Indels
                      486 CTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG

    402
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="C9"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40.6; D. Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                    Chlamydomonadaceae; Chlamydomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 CAAGAAGAGCAAGGCAGCTACATGAT 379
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Chlamydomonas reinhardtii
                                                                                                                                                                                                                                   AV392783.1 GI:6546999
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Hordeum.
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/dev_stage="adult, heading stage"
/clome_lib="K. Sato unpublished cDNA library; Hordeum
vulgare subsp. spontaneum top three leaves adult, heading
360 CTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACGACGACGACACAG
                                                                                               424 CCAGTITGCAGICCACCAICCAGCGCTCAATGGCAIGTACTCGAGCGACCATAGCCCCAT 365
                                                                                                                                     479
                                                                                                                                                                        364 CTCACCGCGCAGGGGGGCTAAGTAGCCTTACAGGTTGCAGCTCAGCTCAGCAGAACACGAA 305
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                                                                                                                                                                                                                                                                                                                                                AV835132 K. Sato unpublished cDNA library: Hordeum vulgare subsp. spontaneum top three leaves adult, heading stage Hordeum vulgare subsp. subsp. spontaneum cDNA clone bah24018, mRNA sequence.
                                                                                                                                 420 AATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGAGAACAACTCTTCCCGCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1. Kurashiki, Okayama 110-0046, Japan
Email: kazeato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp,
sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct
submission;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  database:http://www.shigen.nig.ac.jp/barley/Barley.html.
Location/Qualifiers
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/cultivar="H602"
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/gurann="cc-loyu wild type mt+ 41gf.
/db.xref="taxon:3053"
/clone lib="c. reinhardtii CC-1690, Stress II (normalized
/clone lib="c. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP [MH4 - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
Phys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP +
Rhys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP +
Rhys. 122: 127-135; TAP + Cd (1, 2, 6, 24 hr)
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned incolambda
Zap II (Stratagene) in the EcoRI (5;) and XhoRI (3)
sites. pBluescript II SK- plasmids were excised from the
lambda ZaP clones by superinfection with ExAssist
(Stratagene) Phase. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806.
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebv Grossman, A., Chang, C.-W., Davies, J., Silflow, C. and Stern, D., P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
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/etrain="CC-1690 wild type mt+ 21gr"
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Location/Qualifiers
1. .552
                                                                                                                                                                               Chlamydomonas reinhardtii
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DCMB Box 91000
Duke University
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Tel: 919 613 8159
Fax: 919 613 8177
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3 Kisarazu, Chiba 292-0812, Japan
Email: ynakamudkazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/dev stage="photoautotrophic growth"
/done lib="chlamydomonas reinhardtii C9"
/note="Vector: pBluescriptII SK-; Site_1: EcoKI; Site_2:
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A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433
DON redundant expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
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Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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148; Conservative (
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                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
Email: seqrefégenoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO15CA02NP1.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 584)
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre
P., McDermott, J. P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                         B1727879 584 bp mRNA linear EST 19-SEP-2001 1031095C12.yl C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Chlamydomonas reinhardtii
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
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                                            Vascular Plants. Project: 1031
342 GGAGAACAACTCTTCCCGCTGCTGGGT
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Contact: Charles Hauser
DCMB Box 91000
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                454 ATCTCGCCTCGCCGGCATGACACGCTGCAGGACTGCAATTGCTCAATCTATCCCGGCCAC 513
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                         393
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                                                                    334 IGCGTICGGGAGAACAACICTICCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGGT
                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bisscience Corporation
Clone distribution: MGC clone distribution information can tecond through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2016 row: n column: 18
High quality sequence stop: 567.
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Best Local Similarity 54.4%; Pred. No. 8.2;
Matches 81; Conservative 0; Mismatches 68;
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On Feb 13, 2001 this sequence version replaced gi:12777380.
Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cadex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Invitrogen. This sequence belongs to sequence cluster 4924.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seg=CLOBA006ZGO8RP1kcluster=4924.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
Feng Liang Email: fliang@lifetech.com URL :
Feng Liang Email: cluster.cgi?seg=cLOGBA006ZGO8RP1.
Location/Qualifiers 151 1012 GKKKTTTTWMMADAIMTHTTWWTTWTTYTCTADAWGGGTAKCVAKCCCMCCCCCAMGCTS 953 AL513886 1201 bp mRNA linear EST 08-MAY-2003 AL513886 Home sapiens PLACENTA Home sapiens cDNA clone CLOBA006ZG08 5-PRIME, mRNA sequence. AL513886 432 775 ccákirgéciácegacecececentaréegececéciárácegaréaceáciáceáé 834 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201) Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length, CDNA libraries and normalization gegectrescenceregagaranaratresceregagacececececeragagagacara 92 CCAGGGCCCTGGCGTTCCGGGGTTCTGGAGGACGGCGTGAACTATGCAACAGGGA Gaps CTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACAATACGACGCCAC Query Match
6.6%; Score 40; DB 9; Length 1201;
Best Local Similarity 26.5%; Pred. No. 9.4;
Matches 103; Conservative 104; Mismatches 179; Indels 835 GCCTGATCCCGGCCCTGCACCACCCCGCC 863 Grccarrectagererreacearereece 461

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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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(Dases 1 to 840)
Whitelaw.C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,R., Faw, Fraser,C.M., Budiman,M.A., Bedell,J.A., Roblifing,T., Citek,R.W., Numberg,A., Robbins,D. and Lakey,N.
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107 c 110 g 77 t
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                 Unpublished
Context: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                      Email: tshini@genes.nig.ac.jp
Location/Qualifiers
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Fax: 301-838-0208
Email: whitelaw@tigr.org
    BJ246716.1 GI:20058228
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Contact: Cathy Whitelaw
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
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115:0 107 g 67 t
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58.0%; Pred. No. 12;
live 0; Mismatches 50; Indels
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
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Expressed genes in Triticum aestivum
Unpublished
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Matches 69; Conservative
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EL01T0207B11.b Endosperm_4 Zea mays CDNA, mRNA sequence.
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CD446071.1 GI:31361714
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6.4%; Score 39; DB 14; Length 873;
Best Local Similarity 53.6%; Pred. No. 16;
Matches 81; Conservative 0; Mismatches 70; Indels
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Contact: Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
191 732-445-5735
Email: jlai@waksman.rutgers.edu
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Search completed: December 20, 2003, 06:54:49 Job time : 1558.97 secs

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Sequence Sequence Sequence Sequence Sequence Sequence

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Sequence 25, Application US/08612973
Fatent No. 6150134
GENERAL INPORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-414
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NAME: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNEY. THOMAS E.
REGISFRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 816-4100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHORE: (703) 816-4100
TELECHORE: GABBE PAIRS
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                          US-09-315-850-9
US-08-344-977-3
US-08-344-616-3
US-08-304-686A-3
US-09-315-850-3
US-09-315-850-3
US-08-384-616-11
US-08-344-616-11
US-08-344-616-11
US-08-344-616-13
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US-09-315-850-13
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FEATURE:
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RESULT 1
 Sequence 25, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 27, Appl
Sequence 27, Appl
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Sequence 23, Appl
Sequence 5, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 49, Appl
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Sequence 13, Appl
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                                                                                December 19, 2003, 18:11:23 ; Search time 43.7045 Seconds (without alignments) 6120.154 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-277-597-25

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US-08-470-4268-14

US-09-014-416-4

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US-08-449-093A-15
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Maximum Match 100%
Listing first 45 summaries
                                                             OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
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Best Local Similarity 100.
Matches 606; Conservative
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APPLICANT: MAERTENS, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
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                                                              Length 606;
                                                                                                       0; Indels
                                                              100.0%; Score 606; DB 3; L
100.0%; Pred. No. 8.4e-153;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/08927597
Patent No. 6245503
GENERAL INFORMATION:
                                                                         Query Match
Best Local Similarity 100.
Matches 606; Conservative
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US-08-927-597-25
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Pred. No. 8.4e-153;
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Version #1.25 (EPO)
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PILLING DATE:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYENE, THOMER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: moteled acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENEE: NO
FEATURE:
NAME/KEY: CDS
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480 540

360 420 420 480

| oy O | 541 ATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCTC 600 [| ·- | oy Oy | 121 CTGGAGGACGCGTGAACTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTTATCTTC 180 |
|--|--|----|--|--|
| ç G | 601 TAATAG 606 601 TAATAG 606 | | Oy Dp | 181 CTCTTGGCTTTGCTGTCTGACGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG 240 |
| RESULT Sequence Seque | RESULT 3.71-21 105-00-12-271- | | Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy O | 241 TCCGGGANGTRACCATGTCAACAGTGCACCACTCAACACGGCGCGG 300 241 TCCGGGANGTRACCATGTCACAGTGCAACGTGCACTCAACCACTGGCGGGGGGGG |
| 장 점 | CGGGTT | | ATTC | LILING VALE: ALT-1990 RNEY AGENT INFORMATION: AME: BYRNE, THOMAS E. SGISTRATION NUMBER: 32,205 SFERENCE/DOCKET NUMBER: 1487-10 SCOMMUNICATION INFORMATION: |

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ANTI-SENSE: NO
FEATURE:
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LOCATION:
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                                                                                                                                                                                              Length 723;
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                                                                                                                                                                                            Score 598.2; DB 3;
Pred. No. 1.1e-150;
0; Mismatches 3;
TELEFAX: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                               Query Match
Best Local Similarity 99.5%;
Matches 600; Conservative
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                                                                                                                          NAME/KEY: CDS
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RESULT 5 US-08-612-973-27 ; Sequence 27, Application US/08612973 ; Patent No. 6150134 ; GENERAL INFORMATION:

GACATGATGATGCACACCCCCCCGGGTGCCTGCGTTCGGGAGAACAACTCTTCCCGC 360 o; 61 CGGTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGCCCTGGCGCATGGCGTCCGGGTT 120 180 240 240 241 recescargraceargrenceaaceacrecrecaacreaacreaagearrerargaegeages 300 120 09 9 181 CICTIGGCITITIGCIGICCTGICIGACCGTICCAGCTICCGCTTAIGAAGTGCGCAACGIG 1 ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGGCTTCGCCGACCTCGTGGGGTACATT APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCESS:
ADDRESSED: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A. Gaps .; 0 Query Match 98.6%; Score 597.4; DB 3; Length 636; Best Local Similarity 99.8%; Pred. No. 1.7e-150; Matches 598; Conservative 0; Mismatches 1; Indels 0; COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPARATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION NUMBER: 32,205
ATTONEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHRACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear mat_peptide 301 g ò

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Query Match
Best Local Similarity 99.8%;
Matches 598; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                              361 TGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACA 420
                                                                                                               ATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTG 480
                                                                                                                                   CAGGACTGCAATTGCTCAATCTTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT 540
GACATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGAGAACAACTCTTCCCGC 360
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                                                                                                                                                                                                                                                                                          541 ATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCT
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APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUT
APPLICANT: BUSE, MARTYNOFF, GUT
TILLE OF INVENTION: PROFIEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/927,597
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRER:
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application US/08927597
Patent No. 6245503
GENERAL INFORMATION:
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TELERAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANI
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STATE: VIRGINIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
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LOCATION:
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; LOCATION:
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APPLICANT: MAERTENS, GERT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYER, GUY
APPLICANT: BUYER, GUY
APPLICANT: BUYER, GUY
APPLICANT: BUYER, DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
CONTRY: US.A.
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   636;
   Length
                                                            Indels
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APPLICATION NUMBER: US/08/612,973 FILING DATE: 11-MAR-1996
Score 597.4; DB 3;
Pred. No. 1.7e-150;
0; Mismatches 1;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTC 180
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           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MARTENS, GERT
APPLICANT: BARTENS, GERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/927,597
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
91.7%; Score 556; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 1.8e-139;
Matches 556; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIPECATION:
CLASSIPECATION:
PRIOR APPLICATION NUMBER: US 08/612,973
APPLICATION NUMBER: US 08/612,973
TILING DATE: 11-MAR-196
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOWAS E.
REGISTRATION NUMBER: 32,205
RESTRATION NUMBER: 1487-10
TELEPOMMUNICATION INFORMATION:
TELEPOMENCATION (703) 816-4100
TELEPAK: (703) 816-4100
TELEPAK: (703) 816-4100
TELEPAK: (703) 816-4100
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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1..555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                        CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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HYPOTHETICAL: N
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6245503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
US-08-927-597-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE: ARRACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STAMDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGATGATGAACTGGT 556
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1..555
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                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
US-08-612-973-23
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RESULT 8 US-08-927-597-23 ; Sequence 23, Application US/08927597

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                                                                         Length 795;
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                                                                      Score 516.2; DB 3;
Pred. No. 8.5e-129;
0; Mismatches 3;
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                                                                      Query Match
Best Local Similarity 88.9%;
Matches 600; Conservative
LOCATION:
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US-08-612-973-5
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                                                                                                      301 GACATGATCATGCACACCCCGGGTGCGTGCCTGCGTTCGGGAAACAACTTTCCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARITER GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROFFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROFFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROFFIES
CORRESPONDENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: VIRGINIA GLEBE KOAD
STATE: VIRGINIA
COUTRY: U.S.A.
ZIP: 22201-471-471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILLING DATE: 11-MR-1996
CLASSIPICATION NUMBER: 1497-10
REGISTRATION NUMBER: 1487-10
TELEPAN: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
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Patent No. 6150134
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NAME/KEY:
LOCATION:
FEATURE:
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US-08-612-973-5
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                469 CATGAGAGGGTGCAGGACTGCAATTGCTCAATCCTGGCCACATAACGGGTCACGT
                                                                                    US-08-612-973-47

US-08-612-973-47

Sequence 47, Application US/08612973

Sequence 47, Application US/08612973

Sequence 47, Application US/08612973

Sequence 47, Application US/08612973

GENERAL INFORMATION:
APPLICANT: BUXBE, MARITONE, GUY
APPLICANT: BUXBE, MARIE-ANGE
TITLE OF INVENTION: PROFIEID HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROFIEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
INUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:
ADDRESSEE: MIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: 22201-4714
COUNTY: 0.5.A.
COMPUTER: 12201-4714
COMPUTER: ENDABLE FORM:
MEDIUM TYPE: 10Ppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC COMPATIBLE
OFERATION NUMBER: 1956
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 1487-10
TELECHONE: (703) 816-4000
TELECHONE: (703) 816-4000
TELECHONE: (703) 816-4000
TELECHOL PARKET TO NOW A 7:
SEQUENCE CHARACTRESTICS:
SEQUENCE CHARACTRESTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local Similarity 88.8%; Pred. No. 7.1e-128;
Matches 597; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                     CTCCGGATCCTCTAA 603
                                                                                                                                                                                                                                           CICCGGAICCCACAA 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2082 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-612-973-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.2%; Score 516.2; DB 3; Length 795; 88.9%; Pred. No. 8.5e-129; tive 0; Mismatches 3; Indels 72
                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATACGACGCCACGTCGAT------
                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNDRER:
FILING DATE: 11-WAR-1996
ATTORNEY/AGENT INFORWATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4000
TELEFAX: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.9
Matches 600; Conservative
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1..789
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1..792
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ANTI-SENSE: NO
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; LOCATION: 1
US-08-927-597-5
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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304 ATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGAGAACAACTTTCCCGGTGC 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCGTCGGCGCCCCCCTAGGGGCGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 GAGGACGCCGTGAACTAIGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTAICTTCCTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 GAGGACGCGTGAACTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGACGCCACGTCGATTTGCTCGTTGGGCGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 riedcirirecterictercreacerrecaecricescriareaagrececaacerere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.7%; Score 513.2; DB 3;
88.8%; Pred. No. 7.1e-128;
iive 0; Mismatches 3;
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR.1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 1487-10
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4100
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4100
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TENEGRAPE DAGE PAIR
TYPOTHETICAL: NO
ANTI-SENSE: NO
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Best Local Similarity 88.8
Matches 597; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-08-927-597-47
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                                                                                                                    CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGATGGCGTCCGGGTTCTG 123
                                                                                                                                                                              TIGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC 243
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                                                                                                                                                                                                                                                                                                                                                GGGATGTACCATGTCACGAACGACTGCTCCAACTCCATGGTTTGTGTATGAGGCAGCGGAC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC 591
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                                  CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG
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               TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGGTACATTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47, Application US/08927597

Batent No. 6445503

GENERAL No. 6445503

GENERAL MARRIENS, GEERT

APPLICANT: BOSMAN, FONS

APPLICANT: BOSMAN, FONS

APPLICANT: BUYSE, MARTHOFF, GUY

APPLICANT: BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE

TITLE OF INVENTION: PORTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIE: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
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STREET: 11
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US-08-927-597-47
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532 GCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC 591
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Sequence 49, Application US/08927597

Patent No. 6245503

GENERAL INFORMATION:
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: BENERAL
APPLICANT: PROPERING HORDING FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF UNENTING WANDERS:
ADDRESSEE: USE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF T
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                                                                                                                                                                                                                                                                                   244 GGGATGTACCATGTCACGAACGACTGCTACCAACTCAAGCATTGTGTATGAGGCAGCGGAC
                                                                                                                                                                                                                                                                                                                 ATGATCATGCACACCCCCGGGGTGCGTGCCTTCGGGAGAACAACTCTTCCCGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                         <u>daddacddcddadddadddaddadaaaatatdcccddatagctctritctctarctrcctc</u>
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PERTORIN RELEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 CGACGCCACGTCGAT-----
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CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-08-927-597-49
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                                                                                                        591
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                             532 GCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MAERTENS, GEERT
APPLICANT: MAERTENS, GEERT
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: POTIEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

84.7%; Score 513.2; DB 3; Length 2433;
Best Local Similarity 88.8%; Pred. No. 7.5e-128;
Matches 597; Conservative 0; Mismatches 3; Indels 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: AUXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZURIER: VIRGINIA
COMPUTER: EDADY disk
COMPUTER: EDADY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CLASSIFICATION NOWBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION INFORMATION:
NAME: BYRNE, THOMAS E.
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGHAL
TELECAMINICATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGHAL
TYPE: nucleic cid
TYPE: nucleic cid
TYPE: nucleic cid
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 49, Application US/08612973
Patent No. 6150134
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LOCATION: 1..2427
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LOCATION: 1..2
FEATURE:
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ANTI-SENSE: NO
FEATURE:
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US-08-612-973-49
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US-08-612-973-49
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                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROFFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROFFIES FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ARLINGTON
STATE: 1100 NOATH
CUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
CURRENT FORDICATION NUMBER: 1100 NOAME: BYRNE, THOMAS E.
CLASSIFICATION NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                               RESULT 15
US-08-612-973-7
; Sequence 7, Application US/08612973
; Patent No. 6150134
                                                                                  1015 CGGATCCCACAA 1026
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TYPE: nucleic acid
STRANDEDNESS: single
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                                          592 CGGATCCTCTAA
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LOCATION:
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, LOCATION:
US-08-612-973-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 ITGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCCGGGTTCTG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 GGGATGTACCATGTCACGAACGACTGCTCCAACTCCAAGCATTGTGTATGAGGCAGCGGAC 654
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                             FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYENE, THOMBER 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4000
TELEFAX: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US 08/612,973
                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2433 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 597; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: mat_peptide
; LOCATION: 1..2427
US-08-927-597-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 1..2430
FEATURE:
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ANTI-SENSE: NO
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Search completed: December 20, 2003, 07:03:12 Job time: 46.7045 secs

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December 19, 2003, 16:55:48; Search time 2408.07 Seconds (without alignments) 10804.703 Million cell updates/sec
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636
1 ATGTTGGGTAAGGTCATCGA.....ATCACCACCATCACTAATAG 636
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                      2888711 seqs, 20454813386 residues
                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_htg_inv:*
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em_htg_pln:*
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | 39 Se 7339 2776 | 5028 | 37 5 7338 | AX452774 Sequence | AX685026 Sequence | AR157336 Sequence | AX452770 Sequence AX685022 Sequence | A48685 Sequence 23 | AR157337 Sequence AX452772 Sequence | AX685024 Sequence | A48667 Sequence 5 AR157325 Sequence | AX452754 Sequence | Ax685006 Sequence A48709 Sequence 47 | AR157350 Sequence | AX452/30 Sequence AX685048 Sequence | A48711 Sequence 49 | AX13/331 Sequence AX452798 Sequence | AX68505 | AB0084 | AB0084 | A48669 | AR15732 | AX68500 | AF1650 | AB008445 Hepatiti | AB008446 | ABO49096 Hepatiti | AF165056 Hepatiti | M74813 Hepatitis C AB008447 Hepatitis | . TTS | DNA linear PAT 07-MAR-1997 85. | | and Buyge, M. |
|-------------|---------------|--------------------------------|-------------|--------------|-------------------|-------------------|-------------------|--|--------------------|--|-------------------|--|-------------------|---|-------------------|--|--------------------|--|---------|----------|----------------------|--------|--------------------|---------|----------|-------------------|----------|----------------------|-------------------|--|-----------|--|---|---|
| SOPPE STATE | Ω | A48689 AR157339 AX452776 | 000 | 733 | AX452774 | ~1 | AR157336 | AX452770 AX685022 | 48685 | AR157337 AX452772 | X685024 | A48667 AR157325 | X452754 | X685006 48709 | AR157350 | X685048 | 48711 | AX452798 | X685050 | AB008442 | AB008443 AF207766 | 48669 | R157326 *452756 | X685008 | AF165052 | AB008445 | AB008446 | AB049096 HCVPOLYP | AF165056 | HPCNS1SPJ AB008447 | ALIGNMENT | 636 bp tr WO960438 | | ., De, M.G. and |
| | DB I | 999 | | | | | | | | | | 4 4 9 9 | | | | | | 9 9 | 4 | | 14 | | | | 14 | | ٧. | v. v | ٠, | 1 4 4 4 | | р В | 70470 | E. (|
| | Length | 636 636 636 | m (| \circ | 0 | \circ | 10 | \sim | a o | o o | 9 | თთ | 000 | 8 7 | 80 | 88 | 43 | າຕ | 29 | 29 | 22 | 63 | നം | 63 | 37 | 567 | 29 | 2 C | 38 | н б | | fro | 3 | ied. 1 to 63 G., Bosm |
| · de | Query | 100.0 | 100. | 93. | 93. | 93. | 93. | 93. | 87. | 87. | 87. | c c | 81. | 80. | 80. | 80. | 80. | 80. | 80. | 72. | 72. | 71. | 71. | 71. | 71. | 71. | Η. | | , , | 71.2 | | | . 444 | unclassified. 1 (bases 1 to 636) Maertens, G., Bosman |
| | Score | 999 | | πον | 597.4 | סס | 597 | 597 | 556 | 556 556 | 556 | 515 | 515 | 515 512 | 512 | 512 | 512 | 512 | 512 | (U) | 459.2 | u) | U1 U |) U) | 456 | 454.4 | 54. | 5 4 7 4 | 54 | 452.8 | | A, () A, (| | |
| | Result No. | -1 01 m | 4" L | nω | 7 | ထတ | 10 | 11 | 13 | 14 | 16 | 17 | 19 | 21 | 22 | 24. | 25 | 27 | 8 6 | 30 | 31 | 33 | 34 25 | 36 | 37 | 9 6 | 40 | 14.4 | 43 | 4 4 4 5 | | RESULT 1 A48689 LOCUS DEFINITION ACCESSION | VERSION KEYWORDS SOURCE ORGANISM | REFERENCE AUTHORS |

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Unclassified.
       Sequence 27 : AR157339 AR157339.1 C
AR157339
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                                           Unknown
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TITLE
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    INNOGENETICS NV (BE)
Other publication AQ 2172273 960215
Other publication AU 3382495 960304.
Location/Qualifiers
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                                                                                                            1 (bases 1 to 636)
Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Wirlied hepatitis C virus envelope proteins for diagnostic
therapeutic use
patent: US 6245503-A 27, 12-JUN-2001;
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Best Local Similarity 100.0%; Pred. No. 6.4e-130;
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Sequence 27 f
AX452776
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DEFINITION
ACCESSION
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IMHTPGCVPCVRENNSSRCWVALTFTLAARANASVPTTIRRHVDSQLFTISPRRHETV
                                                                                                                29-MAR-2003
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| QY 421 ATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTG 480 DD 421 ATACGACGCCACGTCGATTCCCCAGCTGTTCACCATCTCGCCCGCGCGCG | RESULT 5 A48687 LOCUS A48687 LOCUS ACCESSION A48687 | THERAPEUTIC UNG PURITIES OF ALCOLOGY THERAPEUTIC UNG AL PATENTIC NV (BE) INNOGENETICS NV (BE) Other publication AU 3382495 960304. S. Location/Qualifiers 1. : .60 / organism="unidentified" //mol_type="genomic DNA" //db_Aref="taxon:32644" 1. : .60 / location/Canamed protein product" //codon_start=1 //protein_da="CAA03136.1" | CGPADLVGYIPLVGAPLGGAA TVPASAYEVRNVGGMYHVTNN PTLAARNASVPTTTIRRHVDN WSPTTALVVSQLLRIL" 7 t | Query Match 93.9%; Score 597.4; DB 6; Length 606; Best Local Similarity 99.8%; Pred. No. 2e-121; Indels 0; Gaps 0; Matches 598; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Oy 1 ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGTTTCGCCGACCTCGTGGGGTACATT 60 1 2 2 2 2 2 |

| Db 181 CTCTTGGCTTTGCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG 240 Qy 241 TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCGGG 300 241 TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGG 300 Qy 301 GACATGATCATGCACACCCCCGGGTGCGTTCGGGAACAACTCTTCCCGC 360 Db 301 GACATGATCATGCACACCCCCGGGTGCGTTCGGGAAACAACTCTTCCCGC 360 Oy 361 TGCTGGGTAGCACACCCCCGGGTGCGTTCGGGAAACAACTCTTCCCGC 360 Oy 361 TGCTGGGTAGCGTCACCCCCAGGTCGCTTCGGCAACGTCCCCCACCACGC 360 Oy 421 ATACGACGCTCACCCCCAGCTCGCAGCTAGGAACGCTCCCCCCCC | 481 CAGGACTGCAATTGCTCAATCTGGGCACATAACGGGTCACCGTATGGGAT 541 ATGATGATGACTGCTCCAACTGCTCCGGCCACATACGGGTCACCGTATGGCAT 541 ATGATGATGATGAACTGGTCGCTACAACGGCCCTGGTGGTATCGCAGCTCCTCCGGATCGT 685026 685026 CUS AX685026 AX68 | Purified Hepatitis C virus therapeutic use Patent: WO 02055548-A 25 18 INNOGENETICS N.V. (BE) Location/Qualifier 1. 606 /organism="Hepatit /mol_type="genomic/db_xref="caxon:11 1. 603 /note="unnamed pro/codon start="1 /rote" codon start="1 /protein_id="CADBG" /translation="MGK VNYATGNIPGGSFIFILI IMHTPGCVPCVRENNSSR ODCNCSIYPGHITGHRMA | Matches 1600 /product="unnamed" SE COUNT 109 a 193 c 167 g 137 t JOHEN MATCH 93.9%; Score 597.4; DB 6; Length 606; Best Local Similarity 99.8%; Pred. No. 2e-121; Matches 598; Conservative 0; Mismatches 1 AIGTIGGGTAAGGTCATCGATACCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT | Db |
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| | AX452774 AX452774 LOCUS DEFINITION Sequence 25 from Patent EP1211315. VERSION AX452774. VERSION AX452774. G1:21712459 SOURCE Hepatitis C virus ORGANISM Hepatitis C virus ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepativirus. Hepativirus. AUTHORS Maertens, G., Bosman, F., de Martynoff, G. and Buyse, M.A. TITLE AUTHORS Maertens, G., Bosman, F., de Martynoff, G. and Buyse, M.A. TITLE AUTHORS TITLE AUTHORS Location/Qualifiers Location/Qualifiers Location/Qualifiers And Lype="genomic DNA" | CDS 1.603 (db xref="taxon:11103" (note="unnamed protein product" (codon start=1 | ATGTTGGGTAAGGTCATCGATACCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT | 121 CTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCT 180 181 CTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCGGCTTATGAAGTGCGCAACGTG 240 |

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1 (bases 1 to 723)
Maettens G., Bosman,F., De Martynoff,G. and Buyse,M.-A.
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AYYSMVGNWAKVLIVMLLFAP"
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Patent: WO 9604385-A 21 15-FEB-1996;
INNOGENETICS NV (BE)
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Purified Hepatitis C Virus envelope proteins for
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Viruses; sgRNA positive-strand viruses, no
Hepacivirus.
93.9%; Score 597; DB 6; L£
100.0%; Pred. No. 2.5e-121;
ive 0; Mismatches 0;
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Patent: WO 02055548-A 21 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
1. 723
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VNYATGNLPGCSFSIPLLALLSCLTVPASAYEVRNVSGMYHVTNDCSNSIVYEAADM
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QDCNCSIYPGHITGRRWAWDWMNWSPTTALVVSQLLRIPQAVDMVAGAHWGVLAGL
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VNYATGNLPGCSFSIFLLALLSCLTVPASAYEVRNVSGMYHYTNDCSNSSIYYEAADM
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87.4%; Score 556; DB 6; Lk
Best Local Similarity 100.0%; Pred. No. 2.7e-112;
Matches 556; Conservative 0; Mismatches 0;
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                              /mol_type="genomic DNA
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QDCNCSIYPGHTGHTRNAMDMMNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGL
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100.0%; Pred. No. 2.5e-121;
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Maertens, G., Bosman, F., De, M.G. and Buy
PURIFIED HEPATITIS C VIRUS ENVELOPE PRC
THERAPEUTIC USE
PATENT: WO 9604385-A 23 15-FEB-1996;
INNOCENTICS NOV (BE)
Other publication AU 3382495 960304.
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Sequence 23 from Patent WO9604385.
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A48685.1 GI:2302398
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
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100.0%; Pred. No. 2.7e-112;
tive 0; Mismatches 0; Indels
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1. :558
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HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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(c) 1993 - 2003 Compugen Ltd.
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                                                                                                        AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. C The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by c arrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV for vaccinating humans against HCV, for in vitro detecting one or antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are not an antibut human sera than those isolated by known
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            s - in presence of disulphide bond cleavage agent, to proteins suitable for direct use in vaccines or diagnostic
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HVV single or specific oligomeric recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV singles or for immunising humans vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for this virto monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                                                                                                                                                                                                               Hepatitis C virus, HCV, El protein; E2 protein; infection; gene; virucide; immunostimulant; vaccine; ds.
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                                                                                                                                                                             Hepatitis C virus clone HCCI40 El protein coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2001; 2001US-260699P.
30-AUG-2001; 2001US-315768P.
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   DNA; 636
                                                                                                                            (first entry)
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AAL48928 standard;
                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
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invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serctyping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known
                                                                                                                                                                                           C; 167 G; 137 T; 0 other;
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Matches 598; Conservative
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                                                      TCCGGGATGTACCATGTCACGAACGACTGCTCCCAACTCAAGCATTGTGTGTATGAGGCAGCG
                                                                                                    CAGGACTGCTATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT
                                                                                                                                                                                                                                                                                                        ATGATGATGATGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCGGGATCGTG
               CTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG
                                     TCCGGGATGTACCATGTCACGACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
                                                                                     GACATGATCATGCACACCCCGGGTGCGTGCCTTGCGTTCGGGAGACAACACTCTTCCCGC
                                                                                                                                      TGCTGGGTAGCGCTCACCCCCACGCTCGCAGGTAGGAACGCCAGCGTCCCCACCACGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purifying recombinant hepatitis C virus (HCV) B1 and B2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic
                                                                                                                                                                                                                                                                                                                                            636
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  DB 17; Length 606;
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                                                     Indels
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Score 597.4; DB 17
Pred. No. 2.6e-148;
                                                  0; Mismatches
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Sequence 723 BP; 126 A; 220 C; 208 G; 169 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligometic recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines useful for inducing HCV-specific antibodies or for immunising humans against HCV The recombinant HCV El and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for the view monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTTGGCTTTTGCTGTCCTTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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virucide; immunostimulant; vaccine; ds.
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                                                                                                                                                                                                                Buyse
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99.8%;
                                                                                                                                       11-JAN-2001; 2001US-260699P.
30-AUG-2001; 2001US-315768P.
                                                                                                              11-JAN-2002; 2002WO-EP00219.
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                                                                                                                                                                                  (INNO-) INNOGENETICS NV
                                                                                                                                                                                                             Maertens G, Bosman F,
                                                                                                                                                                                                                                         2002-599657/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                           from HCV infection
                             Hepatitis C virus.
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AATI2704-T12709 and AATI2961-T12974 represent hepatitis C virus (HCV) E1 cand E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. C in vectors for the production of recombinant E1, E2, and E1/E2 proteins. C invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV c antibodies in a sample, and in a serotyping assay for detecting one or antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are mer reactive with human sera than those isolated by known
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ATACGACGCCACGTCCGATTCCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTG
                                 CAGGACTGCAATTGCTCAATCTACCGGCCACATAACGGGTCACCGTATGGCTTGGGAT
                                                                                                                                                                    ATGATGATGAAGTGGTCGCCTACAAGGCCCTGGTGGTATCGCAGCTGCTCCGGATCGT
                                                                                                                                                                                                                                                                                              Purifying recombinant hepatitis C virus (HCV) E1 and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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               Gaps
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              Indels
      Pred. No. 3.5e-148;
Mismatches 0;
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               597; Conservative
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      Best Local Similarity
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inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV The recombinant HCV E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising ontibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
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                                                                                                                                                                                                                                                                                                                                           Example 2; Page 173-174; 243pp; English
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV El and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for
TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTGTATGAGGCAGCG 300
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                                                                                                                                                                                    421 ATACGACGCCACGTCCAAGTTCCCAAGTTCACCATCTCGCCTCGCCGGCATGACACGGTG
                                                                                                                                                                                                                                                                        181 CAGGACTGCAATTGCTATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT
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                                                                                                                                                            361 recreserrence concentrates and reconsider and reconsider and reconsider.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus clone HCCI38 Bl protein coding sequence.
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30-AUG-2001; 2001US-315768P.
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AAL48926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATI2704-T12709 and AATI2961-T12974 represent hepatitis C virus (HCV) El cand E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant El, E2, and El/E2 proteins. Cc in vectors for the production of recombinant El, E2, and El/E2 proteins. Cc The recombinant proteins are purified by a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage agent, after 1ysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detecting one or antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed El, E2 and El/E2, and eliminates contaminating proteins. Antigens isolated using this method are mentod preserved by known are reactive with human sera than those isolated by known
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                                                                                                                        HCV, E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purifying recombinant hepatitis C virus (HCV) B1 and B2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        De Martynoff G, Maertens
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Best Local Similarity 100.0%; Pred. No. 2.3
Matches 556; Conservative 0; Mismatches
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                                                       (first entry)
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                                                                                                                                                                                                                      Hepatitis C virus.
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                                                       24-SEP-1996
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94EP-0870132

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serotype; reversed phase hybridisation assay; genotype; antigen; sera;
in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequencis a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                        CTGGAGGACGCCTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTC
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                                                                                                                                                                          CCGCTCGTCGCCCCCCCTAGGGGGCGCTGCCAGGGCCCCTGGCGCATGGCGTCCGGGTT
                                                                                                                                                                                                                          CTGGAGGACGCGTGAACTATGCAACAGGGAATTTGCCCCGGTTGCTCTTTCTCTATCTTC
                                                                                                                                                                                                                                                                           CTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG
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                                                                                                                                                  ATGITGGGTAAGGTCATCGATACCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT
                                                                                                   Gaps
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0
                                                                         Length 561;
                                                                                                 0; Indels
                                                  Sequence 561 BP; 103 A; 176 C; 155 G; 127 T; 0 other;
                                                                        87.4%; Score 556; DB 24; L
100.0%; Pred. No. 2.3e-137;
ive 0; Mismatches 0;
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Matches 556; Conservative
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                                                                         Query Match
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant El, E2, and El/E2 proteins. The recombinant proteins can then be isolated using a method of the construct.

The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in virto detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed El, E2 and El/E2, and eliminates contaminating proteins. Antigens isolated by known
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                                                                                                   CGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT
                                                                                                                                                     Hepatitis C virus E2 protein related coding sequence SEQ ID NO: 47.
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30-AUG-2001; 2001US-315768P.
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                                                                               CATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACGT
                                                                                                   72;
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Best Local Similarity 89.2%; Pred. No. 1.8e-126;
Matches 597; Conservative 0; Mismatches 0; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus clone HCCI10A El protein coding sequence.
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GCTTGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
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                                                                                                                                          BP
                                                                                                                                          AAT12973 standard; DNA; 2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 80.5%;
Best Local Similarity 89.2%;
Matches 594; Conservative C
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                                                                                                                                                                                                                      HCV El construct HCCI65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buyse M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-129401/13.
                                                   597
                                                                            699
                                                                                                                                                                                                                                                                                                 Hepatitis C virus.
                                                   CGGATC
                                                                          664 CGGATC
                                                                                                                                                                                                                                                                                                                         WO9604385-A2.
                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                            31-JUL-1995;
                                                                                                                                                                                            24-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bosman F,
                                                   592
                                                                                                                                                                  AAT12973;
 532
                                                                                                                 RESULT 12
                                                                                                                               AAT12973
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                                                                                                                                                                         The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV El and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients sufféring from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCCGCATGGCGTCCGGGTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGACGCCGTGAACTATGCAACAGGGAATTTGCCCCGGTTGCTCTTTCTCTTATCTTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   72;
                                                                                                                                                                                                                                                                                                                                                                           Length 2082;
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                Sequence 2082 BP; 366 A; 634 C; 600 G; 482 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                          Score 512; DB 24;
Pred. No. 1.4e-125;
0; Mismatches 0;
                                                                                                                                                    Example 2; Page 206-209; 243pp; English
                         Buyse M;
                                                                                                                                                                                                                                                                                                                                                                       80.5%;
                                                                                                                                                                                                                                                                                                                                                                                                   Matches 594; Conservative
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                         Bosman F,
(INNO-) INNOGENETICS
                                                   2002-599657/64.
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                           from HCV infection
                                                             P-PSDB; AA018678
                         Maertens G,
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                                        663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant El, E2, and El/E2 proteins. The recombinant El, E3, and El/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV encloades in a sample, and in a serotyping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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604 GCTTGGGATATGATGATGAACTGGTCGCCCTACAACGGCCCTGGTGTATCGCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGGTACATTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
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                                                                                                                                                 HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                                           243
                                                                                                                 ATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGAGAACAACTCTTCCCGCTGC 363
                                            183
                                                           183
                                                                                          243
               123
                              123
63
                                                                                                                                                                    TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACCACAATA
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                                                                                                         GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
                             criciscicciccitadedeceraceaeccraeccareccareecaracearcae
                                                           TTGGCTTTGCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC
TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATTCCG
                CTCGTCGGCGCCCCCTAAGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTTCTG
                                            GAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCTCTC
                                                                                   CGACGCCACGTCGAT------
                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                 AAT12974 standard; DNA; 2433
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                                              El construct HCCI66
                                                                                                                                                                                                                                                                                                                                             699
                                                                                                                                                                                                                                                                                                                             CGGATC 597
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ANTI2704-T12709 and AATI2961-T12974 represent hepatitis C virus (HCV) El and El Zoretin coding sequence constructs. These sequences are included in vectors for the production of recombinant El, E2, and El, E2 proteins. The recombinant proteins and then be isolated using a method of the cinvention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage or a reduction step with a carrying out a disulphide bond cleavage or a reduction step with a carrying out a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used to antibodies in a sample, and in a serotyping assay for detecting one or antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilisation method preserves the conformation of the recombinantly expressed El, E2 and El/E2, and conformation of the recombinantly expressed El, E2 and El/E2, and conformation of the recombinantly expressed El, E2 and El/E2, and conformation more reactive with human sera than those isolated by known
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                                                    Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2433 BP; 434 A; 745 C; 714 G; 540 T; 0 other;
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Pred. No. 1.5e-125;
0; Mismatches 0;
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De Martynoff G,
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Best Local Similarity 89.2
Matches 594; Conservative
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                                                                                                                                                   535 TTGGCTTTGCTGTCCTGTTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTC
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                                                              475 GAGGACGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCTC
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                                                                     955 GCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCCTGGTGGTATCGCAGCTGCTC 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific Oligomeric recombinant envelope proteins selected from an B1 and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence
                                             591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGGGTAAGGTCATCGATACCTTACATGCGGCTTTCGCCGACCTCGTGGGGTACATTCCG 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is a coding sequence described in the exemplification of the invention.
GCTTGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
                                                                                                                                                                                                                                                                                           Hepatitis C virus E2 protein related coding sequence SEQ ID NO: 49.
                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; El protein; E2 protein; infection; gene;
virucide; immunostimulant; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73;
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Pred. No. 1.2e-122;
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                                                                                                                                                                                                        AAL48940 standard; DNA; 2434 BP.
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89.1%;
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                                                                                                                                 1015 CGGATC 1020
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                                                                                                    CGGATC 597
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Best Local Simi
Matches 594;
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Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic WPI; 1996-129401/13 assays of

Claim 23; Fig 21; 146pp; English.

AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1 and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. C in vectors for the production of recombinant E1, E2, and E1/E2 proteins. C invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are merced for a meaning the number of the number of the human sera than those isolated by known

Sequence 633 BP; 111 A; 192 C; 174 G; 156 T; 0 other;

72; Gaps Score 456.4; DB 17; Length 633; Pred. No. 5.3e-111; 0; Mismatches 11; Indels 72; 71.8%; 86.8%; Query Match 71.8 Best Local Similarity 86.8 Matches 545; Conservative

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Search completed: December 19, 2003, 18:51:21 Job time: 178.828 secs

EST 13-FEB-2002

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and Wilson, K.
Washu Zebrafish EST Project 1998

Unpublished
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
A444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Fax: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Sequencing by: Chandra Tucker and Gregory Niemi DNA
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Gequencing by: Mashington University Genome Sequencing Center
Constitution: RessourcenZentrumPrimarDatenbank, Berlin, Germany
Gweb address: www.rzpd.de)
Trace considered overall poor quality
Seq primer: T3 Ef from Amersham
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy S., Hillier, L., Kucaba, T., Martin, J., Bowers, Y., Person, B., K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Kanler, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
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                                                                                                 509 GCCACATAACGGGTC-ACCGTATGGCTTGGGATATGATGAACTGGTCGCCTACAACG 567
                                                                                                                                                340 dergearcaerdeacraeagrardeeraagecrargargargaaerdeereger 281
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Scorif Site_2: Sal1; This Zebrafish library was
constructed_by Dr. Susan B. Brockerhoff (email:
sbrocker@u.washington.edu) RZPD library number: 760"
a 163 c 115 g 116 t
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fm04e08.yl Zebrafish adult retina cDNA Danio rerio cDNA Clone
IMAGE:4145367 5' similar to TR:Q9PWN4 Q9PWN4 RHODOPSIN. ;, mRNA
449 TCACCATCTCGCCTCGCCGCGATGAGACGGTGCAGGACTGCAATTGCTCATCTATCCCG
                                      Query Match
6.5%; Score 41.6; DB 12;
Best Local Similarity 51.0%; Pred. No. 3.4;
Matches 98; Conservative 0; Mismatches 94;
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1 (bases 1 to 492)

Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Gu,Y., Li,N., Oian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,Y., Li,N., Oian,B., Liu,F., Qu,G., Ren,S., Zhong,Z., Xu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z. Homo sapiens cDNA BM clones
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Contact: Zeguang Han
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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                                                                                                                                                                                                                                       Site_2: sfilB"
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Best Local Similarity 67.2%; Pred. No. 0.0015;
Matches 92; Conservative 0; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                            Length 488;
                                                                                                                                                                                                                                                                                                                                                                                             38; Indels
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10.7%; Score 68.2; DB 9;
Best Local Similarity 72.3%; Pred. No. 4.8e-07;
Matches 102; Conservative 0; Mismatches 38;
                     1. .488
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AV392783 AV192783 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii cDNA clone CM096g04_r 5', mRNA sequence.
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .402
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                                                                                                                                                                                                                                                                                                                        Chlamydomonas reinhardtii
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
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Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
A large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433
non-redundant expressed seguence tags
DNA Res. 6 (6), 369-373 (1999)
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                                                  181 ACCGNACTCGCCTCCCTCTCCGCCCCAGCGCTCGCACCCACGAACG 226
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45.3%; Pred. No. 5.7;
tive 0; Mismatches 179; Indels
                            486 CTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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AV392783.1 GI:6546999
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Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
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vulgare subsp. spontaneum top three leaves adult, heading
                                                             CTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACCACGAC 419
                                                                                                       424 CCAGITIGCAGICCACCATCCAGCGCICAAIGGCAIGIACICGAGCGACCATAGCCCCAI 365
                                                                                                                                               420 AATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCGCCGCGTTGAGACGGT 479
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366 GGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACAATACG
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Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kursahiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp,
Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
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                                         Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
                                                                                                                                                                                            Unpublished
Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                                                                                                                 chauser@duke.edu
BI996341
BI996341.1 GI:16431115
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                            Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 153-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamuskazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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ilarity 45.3%;
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/moil type="mRNA"
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/mucl type="mRNA"
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/clone lib="Vc. reinhardtii II SK-; Site_I: EcoRI; Site_2:
/note="Vector: pBluescript II SK-; Site_I: EcoRI; Site_2:
xhoi; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4 - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
Phys: 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
Phys: 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
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Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebv, F., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in
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Chlamydomonadaceae; Chlamydomonae.
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6.4%; Score 40.6; DB 12; Length 552;
Best Local Similarity 45.3%; Pred. No. 6.2;
Matches 148; Conservative 0; Mismatches 179; Indels 0;
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EST 05-MAY-2003
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BX356664 Homo Sapiens PLACENTA COT 25-NORMALIZED Homo Sapiens CDNA
clone CSODI015YB03 3-PRIME, mRNA sequence.
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                                                                                227 CTTCGCCGTCCGCTGCGTGGGCCACTCGCTGGGCGGCGGCACCGCCGGCTGCCTGTCGAT 286
                                                                                                                                                                                     287 CCTGATGCACCACGACGAGGAGTTTGCGGCGCGCATCTACGGCGGCGGCGTGCCCATGCCGGG 346
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                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ thase 1 to 1201)
Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:/fulllength.invitrogen.com/ InVitroGen Corporation 1600
Http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO15CA02NP1.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
88 c 93 g 398 t 506 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                          342 GGAGAACAACTCTTCCCGCTGCTGGGT 368
                                                                                                                                                                                                                                                                                            347 CAÁGAAGAGCAAGGCAGCTACATGAT 373
                                                                                                                                                                                                                                                                                                                                                                                                                               1201 bp
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Homo sapiens
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// strain="C2-1690 wild type mt+ 21gr"
// db_txref="taxon:3055"
// clone lib="C. reinhardtii CC-1690, Stress II (normalized
// clone lib="C. reinhardtii CC-1690, Stress II (normalized
// lone="vector: Bluescript II SK-; Site_!: EcoRI; Site_2:
// note="vector: Bluescript II SK-; Site_!: EcoRI; Site_2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (MH4 - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr)
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5) and XhoRI (3)
sites. pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with ExAssist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
                                                                                                                                                                                  81727879 SEP-2001
1031095C12.yl C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J. P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031
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                                                                                                                                                                                                                                                                                                                                         Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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    .584
    /organism="Chlamydomonas reinhardtii"

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Pred. No. 6.3;
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                                                     436
342 GGAGAACAACTCTTCCCGCTGCTGGGT
                                                     410 CAAGAAGAGCAAGGCAGCTACATGAT
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DCMB Box 91000
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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Best Local Similarity
Matches 148; Conserv
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/clone="IMAGE:548549"
/tissue type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC_106"
/clone_lib="NHH MGC_106"
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/note="Organ: blood; Vector: poTB7; Site_1: Xho1; Site_2:
/note="Organ: blood; Vector: poTB7; Site_1: Xho1; Site_2:
/note="Organ: blood; Vector: poTB7; Site_1: Xho1; Site_2:
/note="Organ: blood; Vector: poTB7; Site_1: Xho1; Site_2:
/note="Organ: blood; Vector: poTB7; Site_1: Xho1; Site_2:
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/note="Organ: blood; Vector: poTB7; Site_2:
/note="Organ: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vecto
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AGENCOURT 6611605 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5485649
5', mRNA Fequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 1162)
II. However the://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                    915 SSSTITESSBEITESSBETTESSSSSTEBISSSSBESSSSBTGSKSSSBESSSSSS 974
                                                                                                                                                                                                                                                                                                                                                                                      394 AGGAACGCCAGCGACCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTCACC 453
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ilarity 54.4%; Pred. No. 9.8;
Conservative 0; Mismatches 68;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BM918259
BM918259.1 GI:19368638
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1125 SAAAVVAAASSVSVATSSSAAAAAASSAAVSASSSSSVSSAAAASVSSSSVAAVVSAVA 1066
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BX356664
BX356664.1 GI:30378083
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/mol_type="mRNA"
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/tissue type="PLACENTA COT 25-NORWALIZED"
/tissue type="PLACENTA COT 25-NORWALIZED"
/clone_Tip="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="Ist strand CDNA was primed with a NotI-oligo (dT)
/note="Ist strand CDNA was primed with a NotI-oligo (dT)
/note="Ist strand CDNA was primed with a NotI-oligo (dT)
/note="Ist strand CDNA was primed with a NotI and ECOR V
digested with Not I and cloned into the Not I and EcoR V
digested with Not I and slow of the pCMVSPORT 6 vector. Library was normalized."
a RB c 93 g 398 t 506 others
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 TCCCCACCACGACAATACGACGCCAACGTCGATTCCCCAGCTGTTCACCATCTCGCCTCGCC
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Contact: Genoscope
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 BVRY cedex - France
BP 191 91006 BVRY cedex - France
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope Sequence ID : CSODIO15CA02NP1.
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373 CTCACCCCACGCTCGCAGCTAGGAACGCCAGCCACCACCACGACAATACGACGCCAC
                                                                  775 ccchcrocchicocaecececechantebocececechaecoarchechendeche
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                                                                                                                                                  433 GTCGATTCCCAGCTGTTCACCATCTCGCC 461
                                                                                                                                                                                       835 GCCTGATCCCGGCCCTGCACCCCGCC 863
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Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae, Pooideae
, Triticeae, Triticum.
, Triticeae, Triticum.
, Ogihara, Y. and Murai, K.
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BJ246716.1 GI:20058228
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                                                                                                                                                 833
832 SGCSKGKTTKTTTKGTCGTTGAAGASMABGRTWGAGGGGGGCCCCYCSCMCCCCCCYB 773
                                                                                                                                                                                                         332 CCTGCGTTCGGGAGAACACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAG 391
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/dev stage="Feekes' scale 10.5.1"
/clone lib="v. Ogihara unpublished cDNA library, Wh_f"
115 c 107 g 67 t
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                                                                                                                           892 AYBSYTGTGRRWTWTTGSBTGCTYASGSSGMYSSKRKBGKKCCMAYAACSCGAGASCSGT
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58.0%; Pred. No. 14;
tive 0; Mismatches 50; Indels
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
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Unpublished
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                              CTAGGAACGCCAGCGTCCCCACCACGACA 420
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whf25g19"
                                                                                                                                                                                                                                                                                                                                                          Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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BJ246716
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/clone lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized." 194 others
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ALS13886 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA006ZG08
ALS13886
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945 AVSASSSSSAAASVSSSAAVSSSVAAASSSSSSSSVAAASSSSSAAAAVASAVSAAAAV 886
                                                                                            152 ATTIGCCCGGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTC 211
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1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4924.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBANO6ZGOSRP1&cluster=4924.f. Contact
Feng Liang Email : filiang@lifetech.com URL : tolding Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Liangle Li
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                                                       527 GTATGGCTTGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGC
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                                                                                                                                                                          587 IGCTCCGGATCGTGATCGAGGCCAGACACCATCACCACCATCA 629
                                                                                                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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/db_xref="taxon:9606"
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EST.
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CC335916 840 bp DNA linear GSS 16-MAY-2003 OGUAJ60TV ZM_0.7_1.5_KB Zea mays genomic clone ZNWBMa0393124,
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1 (bases 1 to 840)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, A., R., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished
                                       Triticum aestivum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 375)
Ogihara; Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 CCTIACAIGCGGCTTCGCCGACCTCGTGGGGTACAITCCGCTCGTCGGGGCCCCCCTAGG 83
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Best Local Similarity 58.0%; Pred. No. 14;
Matches 69; Conservative 0; Mismatches 50; Indels
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                Triticum aestivum (bread wheat)
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/organism="Zea mays"
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Seg primer: TF
Class: beared ends.
Location/Qualifiers
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CC335916
CC335916.1 GI:30805329
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SOURCE
ORGANISM
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APPLICANT: MAERTENS, GERRT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOYES, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGON
STATE: VIRGINIA
STATE: VIRGINIA
COMPUTER: U.S.A.

ZIP: 22201-4714
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 105/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFTCATION: 11-MAR-1996
CLASSIFTCATION: 11-MAR-1996
CLASSIFTCATION: 11-MAR-1996
TELEKORWANIATION: 1435
ATTORNEY/AGENT INFORMATION:
TELEFONDE: (703) 816-4100
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TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-916-686A-9
US-08-324-977-3
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US-08-315-850-11
US-08-315-850-11
   US-09-127-829-1
US-08-150-204E-96
                                    -08-324-977-9
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Patent No. 6150134
GENERAL INFORMATION:
                                    11167
11167
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11499
16039
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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 .; Search time 45.8681 Seconds (without alignments) 6120.154 Million cell updates/sec
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Sequence 47,
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Sequence 25,
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Sequence 49,
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-927-597-25

US-08-612-972-25

US-08-612-972-21

US-08-612-973-21

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US-08-612-973-23

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US-08-927-597-47

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US-08-612-97-40

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US-08-612-97-40

US-08-927-597-13
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                                                                                                                          December 19, 2003, 18:11:23
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Maximum Match 100%
Listing first 45 summaries
                                                                                        - nucleic search, using sw model
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seq length: 200000000
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65.4
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4443.2
441.6
441.6
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Maximum DB E
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                                                                                                                            Run on:
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CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT 540
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100.0%; Pred. No. 1.7e-157;
:ive 0; Mismatches 0;
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                  SUPERGATES.

SUPERGATION
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TO BE STATEMENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
APPLICATION NUMBER: US 08/612,973
APPLICATION NUMBER: US 08/612,973
APPLICATION NUMBER: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELEPHONIS: (703) 816-4100
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GENERAL INCORMATION:
APPLICANT: BOSMAN. FONS
APPLICANT: BOSMAN. FONS
APPLICANT: BOSMAN. FONS
TITLE OF INVENTION: PORTIEND HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PORTIEND FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PORTIENS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PORTIENS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINA
COUNTRY: U.S.A.
ZIP: Z2201-4714
COMPUTER FRADABLE FORM:
MEDIUM TYPE: FORM:
COMPUTER: IBM PC COMPATIBLE
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Patent No. 6245503
                                                                                                          Query Match
Best Local Similarity 100.
Matches 636; Conservative
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| Qy 541 ATGATGATGACGGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCGTG 600 Db 541 ATGATGATGATCGCTACAACGGCCCTGGTGGTGGTTCGCAGCTGCTCCGGATCGTG 600 Qy 601 ATCGAGGGCAGACACCTACACCACCATCACTAATAG 636 Db 601 ATCGAGGGCAGACACCATCACCACCATCACTAATAG 636 | WESTLY 3 WE-UB-6-179-25 SECURIOR TO 6.150134 PRESENT PRESENT APPLICANT: MARRIESS, GERT APPLICANT: DECHANTON: APPLICANT: DECHANTON: APPLICANT: DECHANTON: APPLICANT: DECHANTON: APPLICANT: DECHANTON: MARRIESS 111 COMBERGE OF SEQUENCESS 111 COMBERGE OF SEQUENCESS 111 COMPUTER: LANGE OF SEQUENC | |

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100.0%; Pred. No. 2.7e-147; Dreds
tive 0; Mismatches 0; Indels
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SOFTWARE: PATENTIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: BYRNE, THOMAS E:
REGISTRATION NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECO
ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON GRAFIE OF CITY: ARLINGTON GRAFIE OF CITY: ALLINGTON GRAFIE OF COMPUTEY: U.S.A. ZIP: Z2201-4714
COMPUTER READABLE FORM: MEDIUM TYPE: FLORPY disk MEDIUM TYPE: FLORPY GISK COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
VANDERHYE P.C.
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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Best Local Similarity 100.
Matches 597; Conservative
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ANTI-SENSE: NO
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LOCATION:
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Sequence 21. Application US/08612973
Patent NO. 6150134
GENERAL INFORMATION:
APPLICANT: MARRTENS, GEERT
APPLICANT: BUYSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
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Pred. No. 2.1e-147;
0; Mismatches 1; Indels 0
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                                         LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 99.8
Matches 598; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                              MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , NAME/KEY: ", LOCATION: 1
US-08-927-597-25
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
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US-08-612-973-21
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                                                                  61 CCGCTCGTCGCCCCCCCCTAGGGGCCCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT 120
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APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYER, MARTYNOFF, GUY
APPLICANT: BUYER, MARTYNOFF, GUY
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE: OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIKERI: ALLO MAKIN CHEEL MACE
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: NUMBER: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
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TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (703) 816-4000
(703) 816-4100
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421 ATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTG 480
                                                                       481 CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGAT 540
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APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARKTNOFF, GUY
APPLICANT: DE MARKTNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESCENDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.9%; Score 597; DB 3; Le
100.0%; Pred. No. 2.7e-147;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                              Sequence 21, Application US/08927597
Patent No. 6245503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 100.
Matches 597; Conservative
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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NAME/KEY:
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US-08-927-597-21
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                                                                        STREE: ALLO NORTH CLEAR AND STREE; STREE: ALLO NORTH CLEAR AND STATE: VIRGINIA COUNTY. U.S.A.

ZIP: 22201-4714

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BR PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN ROS/BS-7,597

FILING DATE: 11-MRR-1996
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: 32,205
FILING DATE: 11-MRA-1996
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. 1.4e-136;
Live 0; Mismatches 0;
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 556; Conservative
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ANTI-SENSE: NO
FEATURE:
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TOPOLOGY: lin
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LOCATION:
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LOCATION:
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Sequence 23, Application US/08927597
Sequence 23, Application US/08927597
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: DE PURIFIED HEBATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                               .
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87.4%; Score 556; DB 3; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.4e-136;
Matches 556; Conservative 0; Mismatches 0; Indels
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           INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 561 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                   ; NAME/KEY: mat_peptide
; LOCATION: 1..555
US-08-612-973-23
                                                                                                                                                                                                                                                  1..558
                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-08-927-597-23
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Patent No. 6245503

GENERAL INFORMATION:
APPLICANT: MAERTERS, GERT
APPLICANT: BUYSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 11100 NORTH GLEBE ROAD

FIRET: 11100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 ATACGACGCCACGTCGAT------
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US-08-927-597-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARTYNOFF, GUY
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
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Pred. No. 8.1e-126;
0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.25 (BPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/POCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                              US-08-612-973-5; Sequence 5, Application US/08612973; Patent No. 6150134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                            541 ATGATGATGAACTGGT 556
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Best Local Similarity 89.2%;
Matches 597; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: VIRGINIA COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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1 ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT 60

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64 CICGICGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGATGGCGTCCGGGTTCTG 123
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                                         4 TIGGGIAAGGICAICGAIACCCITACAIGCGGCIICGCCGACCICGIGGGGIAACAIICCG
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APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FOOR
APPLICANT: BOSMAN, FOOR
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.T.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Inw PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THORMATION:
REJECOMUNICATION NUMBER: 12,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 47, Application US/08612973 ; Patent No. 6150134
                                                                                                                                                                                                                                                               661 Crccccarc 669
                                                                                                                                                                                    CTCCGGATC 597
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
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ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2
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; LOCATION:
US-08-612-973-47
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US-08-612-973-47
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                                                                                       PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REFERENCE/DOCKET NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: NUCleic acid
STRANDEDNESS: single
TYPE: COULDEY: LINEAR
                APPLICATION NUMBER: US/08/927,597
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NAME/KEY: mat_peptide
LOCATION: 1..789
US-08-927-597-5
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HYPOTHETICAL: N
ANTI-SENSE: NO
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NAME/KEY:
LOCATION:
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124 GAGGACGGCGTGAACTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCTCT 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2082;
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89.2%; Pred. No. 6.4e-125;
tive 0; Mismatches 0; Indels
              ALIGNAL TATOMAS E.

REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 1467
REFERENCE/DOCKET NUMBER: 1467
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 47: SEQUENCE CHARACTERISTICS:
LENGTH: 2082 base pairs: TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOCHETICAL: NO
ANTI-SENBE: NO
FERTURE: CDNA
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                                                     32,205
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
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Matches 594; Conservative
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LOCATION:
FEATURE:
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US-08-927-597-47
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                                                                                                                                                                                                                                                                                   ATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGAGAACAACTCTTCCCGCTGC 363
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                                                     124 GAGGACGGCGTGAACTATGCAACAGGAATTTGCCCGGTTGCTCTTCTCTATCTTCCTC
                                                                                                                                                                   TTGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTTTGAAGTGCGCAACGTGTCC
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                                                                                                                                     TTGGCTTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC
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APPLICANT: BOSMAN FONS
APPLICANT: BOSMAN FONS
APPLICANT: BUYER, WARIE-AUGE
APPLICANT: BUYER, MARIE-ANGE
APPLICANT: BUYER, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: US.A.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGACGCCACGTCGAT--------
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/927,597
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-927-597-47; Sequence 47, Application US/08927597; Patent No. 6245503; GENERAL INFORMATION:
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CGGATC 669
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                                                                                                                                                                                                                                                                                                                                                         775 CGACGCCACGTCGATTTGCTCGTTGGGGGGGCTGCTTTCTGTTCCGCTATGTACGTGGGG 834
                                                                                                 PATENT NO. 624504

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION VARIENCES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
STREET: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: EMADALE FROM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
COMPUTER: BANDALE FROM:
COMPUTER: BANDALE FROM:
COMPUTER: DATE:
COMPUTER: DATE:
COMPUTER: DATE:
COMPUTER: DATE:
COMPUTER: DATE:
COMPUTER: PRECATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE:
THING DATE:
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                             244 GGGATGTACCATGTCACGAACGACTGCTCCAACTCCAAGCATTGTGTATGAGGCAGCGGAC
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; Sequence 49, Application US/08927597
; Patent No. 6245503
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                                                                                                                                    Sequence 49, Application US/08612973
; Sequence 49, Application US/08612973
; Patent No. 6150134
; RAPELICANT: MARKTENS, GERT
; APPLICANT: BUYSE, WARIE-NOSE
; APPLICANT: BUYSE, WARIE-NOSE
; APPLICANT: DE MARTYNOFF, GUY
APPLICANT: DE NARTINOFF, GUY
; APPLICANT: DE NARTINOFF, GUY
; APPLICANT: DE NARTINOFF, GUY
; APPLICANT: DE NARTINOFF, GUY
; APPLICANT: DE NARTINOFF, GUY
; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; STREET: 1100 NORTH GLEBE ROAD
; STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
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ZITA: VIRGINIA

COUNTRY: U.S.A.

ZITB: 2201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/612,973
FILING DATE: II-MAR.1996
CLASSIFICATION NUMBER: 35.05
REGISTRATION NUMBER: 32.05
REGISTRATION NUMBER: 32.05
REGISTRATION NUMBER: 32.406
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
FURTHER TOWN FOR SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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80.5%; Score 512; DB 3; 1

Best Local Similarity 89.2%; Pred. No. 6.6e-125;

Matches 594; Conservative 0; Mismatches 0;
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TYPE: nucleic acid
STRANDEDNESS: single
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1..2427
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664 CGCATC 669
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US-08-612-973-49
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                                                                                                                     RESULT 13
US-08-612-973-49
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61 CCGCTCGTCGCCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT 120
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                                                            PAPETELL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUSMAN, FONS
APPLICANT: BUSMAN, FONS
APPLICANT: BUSMAN, FONS
APPLICANT: BUSMAN, FONS
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: 1100 NORTH GLEBE ROAD
COUNTRY: US.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATCHIN DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION NUMBER: 132,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INVERS: 122004
TELECOMMUNICATION INVERS: 132,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INVERS: 136,2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGITGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT
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86.8%; Pred. No. 1.7e-110;
iive 0; Mismatches 11;
                            7, Application US/08612973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 Dase pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.8
Best Local Similarity 86.8
Matches 545; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing-
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COCATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2433 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRATURE:
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Matches 594; Conservative
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Search completed: December 20, 2003, 07:03:15 Job time : 48.8681 secs

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December 19, 2003, 16:55:48 ; Search time 2385.36 Seconds (without alignments) 10804.703 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| % Query Match Length | | 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | A48691 Sequence 29 from Pat A48691 A48691. GI:2302404unidentified unclassified. 1 (bases 1 to 630) Maertens, 6. Bosman, PURIFIED HEPATITIS C THERAPEUTIC USE PATENT: WO 9604385-A |
| sult No. So | 1 1 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 4 4 4 4 4 | RESULT 1 A46691 LOCUS DEFINITION ACCESSION VERGION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE |

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Other publication AU 3382495 960304
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100.0%; Score 630; DB 6; I
Best Local Similarity 100.0%; Pred. No. 4.5e-165;
Matches 630; Conservative 0; Mismatches 0; DNA DNA 630 630 therapeutic use Patent: US 6245503-A 29 12-JUN-2001; 630 bp Sequence 29 from Patent EP1211315. AX452778 160 630 bp from patent US 6245503. Location/Qualifiers /organism="unknown" 175 c 168 g AR157340 Sequence 29 from patent AR157340 AR157340.1 GI:16218274 Unclassified Unknown. 127 RESULT 3
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LHTPGCIPCVQDGNTSTCWTPVTPTVAVKYVGATTASIRSHVDLLVGAATMCSALYVG
DMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMAMDMMNN"
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Purified Hepatitis C Virus envelope proteins for diagnostic
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Patent: WO 02055548-A 29 18-JUL-2002,
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/db_tref="taxon:11103"
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Best Local Similarity 100.0%; Pred. No. 4.5e-165;
Matches 630; Conservative 0; Mismatches 0;
                                Hepatitis C virus
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Hepacivirus.
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C; E; E2/NS1; core protein; envelope protein; nonstructural
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Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Okamoto, H., Tokita, H., Sakamoto, M., Horikita, M., Kojima, M.,
Lizuka, H. and Mishiro, S.
Characterization of the genomic sequence of type V (or 3a)
hepatitis C virus isolates and PCR primers for specific detection
J. Gen. Virol. 74 (Pt 11), 2385-2390 (1993)
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Pred. No. 4.4e-153;
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                                                                                                                                                                                                                                                                                  HPCSTRUCTC 1546 bp ss-RNA linear VRL 27-JUL-1994
Hepatitis C virus core and envelope proteins gene, 5' end of cds.
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Hepacivirus.
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                                       CGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGATGTGCTCTGCGCTCTACGTGGGT
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Choo, D. Richman, K., Han, J.H., Berger, K., Lee, C., Dong, C., Choo, Q.-L., Richman, K., Han, J.H., Barr, P.J., Weiner, A., Bradley, D.W., Kuo, G. and Houghton, M.
Bradley, D.W., Kuo, G. and Houghton, M.
Genetic organization and diversity of the hepatitis C virus Proc. Natl. Acad. Sci. U.S.A. 88 (6), 2451-2455 (1991)
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/ dorganism="Hepatitis C virus"

/ dorganism="Hepatitis C virus"

/ tissue frype="serum"

/ note="specific host (French)"
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/note="encodes core and envelope proteins"
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core protein; envelope protein; structural region.
Hepatitis C virus
Hepatitis C virus
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AHGVSTLTSLFSSGPQQKLQLVKTNGSWHINSTALNCNESINTGFIAGLFYYHKFNST
GCPQRLSSCKPITFFRQGWGSLTDANVTGASADKPYCWHYAPRPCDVVPALNVCGPVY
     993 GGACCCCAGTGACACCTACAGTGGCAGTACGTACGTCGGAGCAACTACTGCTTCGATAC 1052
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99, D- 76133 Karlsruhe, FRG
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1. .226"
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                                                                                                                                                                                                                                                                                                                                                                                                                             core protein; envelope protein; NS1 protein.
Hepatitis C virus
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GIRFATGRIPGCSPSIFLLALESCLIHPAASLEWRNTSGLYVLTNDGSNSIYVEADD
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VGDMCGAVELVGQAFTRRPRHQTVQTCNCSIYFGHLSGHRAMDMMMNSPRAVGNVV
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SRHTOAFAGLFDIGPQQKLQLNVNTNGSWHINGTALNCNRSINTGFIAGLFYYHKFNST
GGPQRLSSCKPITFFRQGWGPLTDANITGPSDDRPYCWHYAPRRCDIVPASSV"
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|mol type="genomic RNA"
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                                                   Submitted (28-JAN-1993) to DDBJ by:
Hiroaki Okamoto
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                   Okamoto, H.
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1053 GCAGTCATGTGGACCTATTAGTAGGCGCGGCCACGATGTGCTCTGCGCTCTACGTGGGGT 1112
                                                                                                                      HCVCENS1 9390 bp RNA linear VRL 17-JAN-1995 Hepatitis C virus genes for core, envelope and NS1 proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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On Jan 24, 1995 this sequence version replaced gi:506489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seelig, R., Weber, P., Seeling, H.P., Ledger, N., Bottner, C. and
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GGKAKICGLYLFNWAVRTKTNLTPLPATGQLDLSSWFTVGVGVGNDIYHSVSRARTRYL
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ö Gaps 0; Query Match 93.0%; Score 585.6; DB 14; Length 9390; Best Local Similarity 96.2%; Pred. No. 1.4e-152; Matches 600; Conservative 0; Mismatches 24; Indels 0; 654

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D17763.1 GI:514395

D01702rotein; C; E1; E2/NS1; NS2; NS3; NS4a; NS4b; NS5a; NS5b.

D01702rotein; C; E1; E2/NS1; NS2; NS3; NS4a; NS4b; NS5a; NS5b.

Heparitis C virus

Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae; VRL 04-FEB-1999 1134 ATATGTGCGGAGCCGTCTTTCTCGGGGAAGCCTTCACGTTCAGACCTCGTCGCCATC 1193 1013 481 541 542 AAACCGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCTTTCAGGACATGG 601 421 TTATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACATCCACGTGCT 361 121 181 241 893 301 Entire nucleotide sequence and characterization of a hepatitis C virus of genotype V/3a J. Gen. virol. 75 (Pt 7), 1761-1768 (1994) GGACCCCAGTGACACCTACACTGGCAGTCAAGTACGTCGGAGCAACCACCGCTTCGATAC ACATGTGTGGGGGTGTCTTCCTCGTGGGACAAGCCTTCACGTTCAGACCTCGTCGCCATC GCAGTCATGTGGACCTATTAGTGGGCGCGCCACGATGTGCTCTGCGCTCTACGTGGGTG TCGTCGGCGCTCCCGTAGGAGGCGTCGCAAGAGCCCTTGCGCATGGCGTGAGGGCCCTTG 122 AAGACGGGATAAATTTCGCAACAGGGAATTTGCCCGGTTGCTCCTTTTCTATTTTCCTTC GCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGCCGATGACG 1 (bases 1 to 48) Sakamoto,M., Akahane,Y., Tsuda,F., Tanaka,T., Woodfield,D.G. linear 9456 bp RNA Hepailtis C virus complete genome sequence. D17763 CITGGGATATGATGATGAACTGGT 625 Sakamoto,M. Unpublished 3 (bases 1 to 9456) Hepacivirus. (sites) Okamoto, H. Okamoto, H. 94292926 602 482 242 302 362 422 62 ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION MEDLINE PUBMED REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS JOURNAL TITLE RESULT HPCEGS q 셤 ò В 엄 ò 염 g 8 임 ò ò QQ 원 ò ò ò ò a

Submitted (27-559-1993) Hitroaki Okamoto, Jichi Medical School, Submitted (27-51993) Hitroaki Okamoto, Jichi Medical School, 329-04, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:0285-44-11(ex.3334), Pax:0285-44-1557)
Location/Oualifiers /organism="Hepatitis C virus" source FEATURES

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HECUSI14CE 1786 bp RNA linear VRL 01-FEB-2000
Hepatitis C virus genes for C, E and E2/NS1, partial cds.
D14309
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Hepatitis C virus
Hepatitis C virus
Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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C; E; E2/NS1; core protein; envelope protein; nonstructural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPCTH85CE 1786 bp RNA linear VRL 01-FEB-2000
Hepatitis C virus genes for C, E and B2/NS1, partial cds.
D14307
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Hepatitis C virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus
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1173 AAACGGTCCAGACCTGTAACTGTTCGCTGTACCCAGGCCATCTTTCAGGACATCGAATGG 1232
                                                                                                                                                                                                                                      Okamoto, H., Tokita, H., Sakamoto, M., Horikita, M., Kojima, M., Iizuka, H. and Mishiro, S. Characterization of the genomic sequence of type V (or 3a) characterization of the genomic sequence of type V (or 3a) bepatitis C virus isolates and PCR primers for specific detection J. Gen. Virol. 74 (Pt 11), 2385-2390 (1993)
GCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGCATTGTGTATGAGGCCGATGACG 932
                                                                   362 ggaccccaggreacaccrargacagregargargargargargaraccaccaggarac
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                                          TTATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACATCCACGTGCT
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C; E; E2/NS1; core protein; envelope protein; nonstructural
protein.
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/organism="Hepatitis C virus"
/mol type="genomic RNA"
/isolate="Th85"
/db_xref="taxon:11103"
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                                 Okamoto, H., Tokita, H., Sakamoto, M., Horikita, M., Kojima, M., Iizuka, H. and Mishiro, S. Characterization of the genomic sequence of type V (or 3a) hepatitis C virus isolates and PCR primers for specific detection J. Gen. Virol. 74 (Pt 11), 2385-2390 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Hepatitis C virus"
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/product="E2/NS1"
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Hepatitis C virus Hepatitis C virus Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus:

SOURCE ORGANISM

REFERENCE AUTHORS TITLE

C Virus

. and Hoyne, P.A. genome of Hepatitis

1 (bases 1 to 9425) Shukla,D.D., Chaturvedi,S., Cao,J.Y. and Complete Nucleotide Sequence of the genom type 3a (CB)

2 (bases 1 to 9425)
Shukla,D.D., Chaturvedi,S., Cao,J.Y. and Hoyne,P.A.
Direct Submission
Submitted (04-FEB-1998) Biomolecular Research Institute, 343, Royal
Parade, Parkville, Melbourne, Victoria 3052, Australia
Location/Qualifiers

source

FEATURES

REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

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SRPSWGPNDPRRRSRNLGKVIDTLTCGFADLMGVIPLVGAPVGGVARALAHGVRALED
GINFATGNLEDGCSFSIFLLAFBCCLIPPASALEMRNTSGGLYITUNDCSNSSIVYEADD
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GCPQRLSSCKPITSFNQGWGPLTDENIIGPSDDKPYCWHINPRPROCKSVPASSY
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/product="C"
851. .1426
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Matches 594; Conservative
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STLEGNPAVASLMAFTASVTSPLTTNQTWFFNILGGWVATHLAGPQSSSAFVVSGLAG
STGGIGLGRVLLDILAGAGGSGALVAFKINGGELPTABDYNULLPAILSPQALVV
GVICAAILRRHVGPGAVOMMNLI. BUNDKSRGHVVSPSDAAARVTALLSSLT
VTSLLRRLHQMINEDYPSPCSDDMLRIINDWVCSVLSDFKSWLSSAKINPALPGLPFIS
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GINRATGNIPPGCSFSIFLLALESCLIHPASLEWRNTSGLYVLTNDCSNSSIVYEADD
GILHTPGCVPCVQNNISITCHTPVTPTVAVRYVGATTASIRSHVDLYQATMGSALX
VGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHLSGHRMANDMMMNWFPALGMAV
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AHATRGLTSLFSVGAQQKLQLVNTNGSWHINSTALNCNESINTGFIAGLFYYHRFNST
GCPQRLSSCKPITFFKQGWGPLTDANISGPSDDKPYCWHYAPRPCKVVPASGVCGPVY
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PCTVNFTLFKVRMFVGGFEHRFTAACNWTRGBRCDIEDRDRSBQHPLLHSTTELAILP
CSFTPMPALSTGLIHLHQNIVDVQYLYGVGSGMVGWALKWEFVILIFLLLADRRVCVA
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SVAATLGFGSFMSRAYGIDPNIRTGNRTVTTGAKLTYSTYGKFLADGGCSGGAYDVII
CDECHAQDATSILGIGTVLDQAETAGVRLTVLATRTPPGSITVPHSNIEEVALGSEGE
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DVVVCATDALMTGYTGDFDSVIDCNVAVEQYVDFSLDPTFSIETRTAPQDAVSRSGRR
GRTGRGRLGTYRYVAPGERPSGMFDSVVLCECYDAGCSWYDLQPAETTVRLRAYLSTP
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LGGVLAALAAYCLSVGCVVIVGHIELGGKPALVPDKEVLYQQYDEMEECSQAAPYIEQ
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DSTVTEQDIRVEEEIYQCCNLEPEARKVISSLTERLYCGGPMFNSKGAQCGDRRCRAS
                                                                                                                                                                                                                                                                                                                                                   /trānslation="MSTLPKPQRKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRL
GVCATRKTSERSQPRRRRQPIPKARQSGGRSWAQPGYPWPLYGNEGCGWAGWLLSPRG
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/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/strain="type 3a (CB)"
/db_xref="taxon:11103"
                                                                                                                                                                                                                                          /product="polyprotein"
/protein_id="AAC03058.1"
                                                                                                                                                                                                                                                                                                                db_xref="GI:2895899"
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AF046866.1 GI:2895898
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GVLPTSFGNTITCYIKATAAANGAGLRDPDFLVCGDDLVVVAESDGVDEDGAALRAFT

RESULT 11
AF04686
LOCUS
DEFINITION
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KEYWORDS

us-09-899-303a-29.rge

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TITLE
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REFERENCE
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Hepatitis C virus
Hepatitis C virus
Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
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TARHTPVNSWLGNIIMYAPTIWVRMVMMTHFFSILGSGEILDRPLDFEMYGATYSVTP
LDLPAIIERLHGLSAFTLHSYSPVELNRVAGTLRKLGCPPLRAWRHRARAGRAKLIAQ
GGKAKICGLYLFNWAVRTKLTPLPRAGQLDLSIWFTVGVGGNDIYHSVSRARTRYL
LLCLLLLTVGVGJEILFARM

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                                                                                                                                                                                                    TCGTCGGCGCTCCCGTAGGAGGCGTCGCAAGAGCCCTTGCGCATGGCGTGAGGGCCCTTG 121
                                                                                                                                                                                                                             814
                                                                                                                                                                  the genome of hepatitis C virus type 3a:
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1 (bases 1 to 9454)
Yamada,N., Tanihara,K., Mizokami,M., Obba,K., Takada,A., Tsustumi,M. and Date,T.
Full-length sequence of the genome of hepatitis C virus comparative study with different genotypes
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                                                                                                       Length 9425;
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iive 0; Mismatches 30;
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GRPWAPADDPRRSRSTMCGYVIDTLTCGFADLMGYTPLVGAPLGGAARALAHGURALES
GRPWAPADDPRRSRSTMCGKVIDTLTCGFADLMGYTPLVGAPLGGGAARALAHGURALED
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GVLPTGFGNTITTCYIKATAAARAAGIRNPDFLVCGDDLVVVAESDGVDEDRATIKAFT
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RSLSSKAINQIRSVWEDLLEDTTTPIPTTIMAKNEVFCVDPAKGGRKÄARLIVYPDLG
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                                                                                                                                                                                                                                                                                                                                        Direct Submission

Direct Submission
Submitted (12-MAR-1994) Takayasu Date, Kanazawa Medical Univercity,
Submitted (12-MAR-1994) Takayasu Date, Kanoku-gun, Ishikawa 920-02,
Department of Biochemistry, Uchinada, Kahoku-gun, Ishikawa 920-02,
Japan (Tel:0762-86-2211(ex.3701), Fax:0762-86-4693)

Location/Qualifiers
Gen. Virol. 75 (Pt 11), 3279-3284 (1994)
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/translation="MSTLPKPQRKTKRNTIRRPQDIKPPGGGQ1VGGVYVLPRRGPRL
GVRATRKTSRBSQPRGRRQPIPARARSEGRSWAQPGVPWPLYGNBGGGWAGNLLSPRG
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GCPHRLSSCKPITSFRQGMGSLTDANISGSSEDKPYCWHYARPRPCTVVPASSV"
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                     Okamoto, H.
Unpublished
Submitted (28-JAN-1993) to
Hiroaki Okamoto
Immunology Division
Jichi Medical School
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0285-44-1557.
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Tochigi 329-04
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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(Mandoto, H., Tokita, H., Sakamoto, M., Horikita, M., Kojima, M.,
Iizuka, H. and Mishiro, S.
Characterization of the genomic sequence of type V (or 3a)
hepatitis C virus isolates and PCR primers for specific detection
J. Gen. Virol. 74 (Pt 11), 2385-2390 (1993)
7504073
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                                                                                                                                                                             TGGGTAAAGTCATCGATACCCTCACGTGCGGATTCGCCGATCTCCATGGGGTACATCCCGC
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C; E; E2/NS1; core protein; envelope protein; nonstructural
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                                                                               Length 9454;
                                                                                                                30; Indels
                                                                           Query Match 91.4%; Score 576; DB 14; Best Local Similarity 95.2%; Pred. No. 6.6e-150; Matches 594; Conservative 0; Mismatches 30;
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TATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACATCCACGTGCTG
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Patent: 10.0046/70-A 21 31-MAY-2000;
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    542 protein product; Protein sequence is
conflict with the conceptual translation

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HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1

CC and B2 protein coding sequence constructs. These sequences are included
in vectors for the production of recombinant B1, B2, and B1/E2 proteins.

CC The recombinant proteins can then be isolated using a method of the
invention. In the method, the envelope proteins are purified by
carrying out a disulphide bond cleavage, or a reduction step with a

CC disulphide bond cleavage agent, after 19sis of recombinant host cells.

CC disulphide bond cleavage agent, after 19sis of recombinant host cells.

The constructs containing the purified HCV envelope proteins can be used

CC for vaccinating humans against HCV, for in vitro detecting one or
antibodies in a sample, and in a serotyping assay for detecting one or
cc more serological types of HCV present in a biological sample.

CC constructs can also be immobilised on a solid substrate and incorporated

CC constructs can also be immobilised on a solid substrate and incorporated

CC the genotype of HCV. The new purification method preserves the

CC conformation of the recombinantly expressed B1, B2 and B1/E2, and

CC and minates contaminating proteins. Antigens isolated using this method

CC are more reactive with human sera than those isolated by known
proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV
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                                                                                                                                                           GAAGACGGGATAAATTTCGCAACAGGAATTTGCCCGGTTGCTCCTTTTCTATTTTCCTT 180
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                                                                1 ATGGGTAAGGTCATCGATACCCTTACGTGCGGATTCGCCGATCTCATGGGGTACATCCCG
                                                                                     1 ATGGGTAAGGTCATCGATACCCTTACGTGCGGATTCGCCGATCTCATGGGGTACATCCC
                                                                                                                                  CTCGTCGGCGCTCCCGTAGGAGGCGTCGCAAGAGCCCTTGCGCCATGGCGTGAGGGCCCTT
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DB 17; Length 630;
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GAAGACGGGATAAATTTCGCAACAGGAATTTGCCCGGTTGCTCCTTTTCTATTTCCTT GAAGACGGGATAAATITCGCAACAGGGAAITTGCCCGGTTGCTCCTTTTCTATTTTCCTT

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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and an El protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunishing humans againt HCV. The recombinant HCV B1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV E1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in viro monitoring of HCV disease or prognosing the response to invitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCGTCGGCGCTCCCGTAGGAGGCGTCGCAAGAGCCCTTGCGCATGGCGTGAGGGCCCTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New therapeutic vaccine compositions comprising at least one purifierecombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans
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100.0%; Pred. No. 4e-192;
ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                           Hepatitis C virus clone HCCI62 E1 protein coding sequence
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601 GCTTGGGATATGATGAACTGGTAATAG 630
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30-AUG-2001; 2001US-315768P.
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                                                                                           DNA;
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                                                                                           AAL48929 standard;
                                                                                                                                                                                                                                                                                        Hepatitis C virus.
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Best Local Si
Matches 630;
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121 TGCTCTGTTCTCTTGCTTAATTCATCCAGCTAGTCTAGAGTGGGGGGAATACGTCTGG 180
                             Compositions comprising at least 5, and pref. 8 or more contiguous nuclectides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning positions 417-957 of the Core/E1 region of HCV subtype 3s, (1i) the region spanning positions 6464-4730 of the NS3 region of HCV type 3; (iii) the region spanning positions 892-529 of the NS3 region of HCV type 3; (iii) the region spanning positions 8021-8215 of the NS5 region of HCV BR36 subgroup of HCV subtype 3s; or (v) an HCV subtype 3c genomic subgroup of HCV subtype 3s or (v) an HCV subtype 3c genomic subgroup of HCV subtype 3s or (v) an HCV subtype 3c genomic isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid. Polypeptides encoded by Ct he nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the Core/E1 region of HCV subtype 3a and is taken from a clone designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCTTTCAGGACATCGAATGGC
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99.4%; Pred. No. 5.5e-162;
iive 0; Mismatches 3;
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    Claim 2; Page 111-112; 404pp; English.
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Best Local Similarity 99.4
Matches 538; Conservative
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GGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGCCGATGAC
                                                                                                                            GTTATTCTGCACACACCCGGCTGCATACCTTGTGTCCCAGGACGGCAATACATCCACGTGC
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                                              GCCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGCCGATGAC
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/product= Core/E1 polypeptide.
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(first entry)
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01-AUG-1995
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483 CATGTGTGGGGCTGTCTTCCTGGGGGGGCCTTCACGTTCAGACCTCGGCCATCA
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CCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGCCGATGACGT
                    303 TATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACATCCACGTGCTG
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93EP-0402019.
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                                                                                               detection; diagnosis;
                                                                                             Hepatitis C virus; HCV; primer; probe; detection; diagnosi classification; immunisation; prophylaxis; serotyping; ss.
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/product= Core/B1 polypeptide.
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                                                                Hepatitis C virus Core/El region.
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Location/Qualifiers 2..541 /*tag= a

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Hepatitis C virus; HCV; primer; probe; detection; diagnosis; classification; immunisation; prophylaxis; serotyping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTCTGTTCTCTTGCTTAATCCATCCAGCAGCTAGTCTAGAGTGGGGGGAACACGTCTGG 180
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                                                                                                                                                                                                                                 Sequence 541 BP; 104 A; 153 C; 145 G; 139 T; 0 other;
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Pred. No. 2.3e-151;
0; Mismatches 23;
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Best Local Similarity 95.7%;
Matches 517; Conservative
93EP-0401099
93EP-0402019
                                                                                               (INNO-) INNOGENETICS NV SA.
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P-PSDB; AAR63279.
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AAQ78031 standard; cDNA; 540

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25-MAR-2003 21-JUL-1995 AAQ78031;

AAQ78031 1D AAQ XX AC AAQ XX DT 25-1 XX

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sequence, may be used as primers to amplify nucleic acid from an isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid. Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the Core/E1 region of HCV subtype 3a and is taken from a clone designated
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                                                                                                                                                 ATGTGTGGGGCTGTCTTCCTCGTGGGACAAGCCTTCACGTCAGACCTCGTCGCCATCAA
                                                                                                                                                                                             ACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCTTTCAGGACATCGAATGGCT
                   ATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACATCCACGTGCTGG
                               New polynucleotide sequences from hepatitis C virus - and related vectors, polypeptide(s) and antibodies, useful for immunisation, treatment, diagnosis and typing of HCV isolates
                                                               ACCCCAGTGACACCTACAGTGGCAGTCAAGTACGTCGGAGCAACCACGCTT
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classification; immunisation; prophylaxis; serotyping; ss
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                                                                                                                                                     CGTCGGCGCTCCCGTAGGAGGCGTCGCAAGAGCCCTTGCGCCATGGCGTGAGGGCCCTTGA
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                                                                          DB 15; Length
                                                                      79.8%; Score 502.6; DB 15; Length 95.6%; Pred. No. 3.5e-151; ive 0; Mismatches 24; Indels
                                    Sequence 541 BP; 106 A; 154 C; 143 G; 138 T; 0 other;
(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                            Best_Local Similarity 95.6
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      301 GACCCCAGTAACACCTACAGTGGCAGTCAGGTACGTCGGGGCAACCACCGCTTCGATACG 360
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Location/Qualifiers
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  the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the Core/El region of HCV subtype 3a and is taken from a clone designated
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                                                                                                                                       Sequence 541 BP; 100 A; 155 C; 148 G; 138 T; 0 other;
                                                                                                                                                                         Query Match
Pest Local Similarity 95.2%; Pred. No. 3.8e-150;
Matches 515; Conservative 0; Mismatches 26;
                                                                                                (Updated on 25-MAR-2003 to correct PN field.)
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Pred. No. 1.2e-149;
0; Mismatches 27;
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                                                                                                                  WO9425601-A2
                                                                                                                                                                                                                                                                                                                                 27-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1993;
05-AUG-1993;
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                                                                                                                                                                                                                                10-NOV-1994
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                                                                                                                                                                                                                          241 TGCTCTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTC
                                                                                                                                                                                                                                                                                    301 ACGTTCAGACCTCGTCGACCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGC
                                                                                GACGGCAATACATCCACGTGCTGGACCCCCAGTGACACTGGCAGTCAAGTACGTC
                                                                                                                                           TGCTCTGCGCTCTACGTGGGTGACATGTGTGGGGGCTGTCTTCCTCGTGGGACAAGCCTTC
                                                                                                                                                                                                                                                                 ACGTTCAGACCTCGTCGCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            envelope 1; core protein; HCV genotyping; antibody; vaccine;
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                                                                                                                                                                                                                                                                                                                                                361 CATCTTTCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGT
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/note= "does not contain start or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hepatitis; ss.
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                                                CATGTGGGGCTGTCTTCCTCGTGGGACAAGCCTTCACGTTCAGACCTCGTCGCCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                    isolate S54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ83883 encodes AAR69672 hepatitis C virus (HCV) envelope 1 (B1) protein isolate S54, both can be used for the diagnosis of HCV infection, and in the prodn. of anti-HCV vaccines, antibodies and antisera. The CDNA may also be used to inhibit the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-nucleotide(s), peptide(s) and proteins, used in diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate S
diagnosis; vaccines; antibodies; antisera; gene inhibition; ss.
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Pred. No. 6.9e-113;
0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 576 BP; 110 A; 156 C; 163 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus envelope 1 gene cDNA isolate S54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/*tag= a
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(first entry)
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19-SEP-1995
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AAQ81882 encodes AAR69671 hepatitis C virus (HCV) envelope 1 (E1) protein isolate S52, both can be used for the diagnosis of HCV infection, and in the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may also be used to inhibit the expression of the HCV E1 gene.
   Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived
oligo-nucleotide(s), peptide(s) and proteins, used in diagnosis
and in vaccines
                                                                                                                                   Sequence 576 BP; 108 A; 153 C; 166 G; 149 T; 0 other;
                                                                                                                (Updated on 25-MAR-2003 to correct PN field.)
                                             Claim 1; Page 72; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
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                                                                                                                                           <u>ATTGTGTACGAGGCCGATGACGTTATTCTGCACACCCGGCTGCATACCTTGTGTCCAG</u>
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                                                                                                                                                                                                                                    TGCTCTGCGCTCTACGTGGGTGACATGTGTGGGGGCTGTCTTCCTCGTGGGACAAGCCTTC
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                                                                                                                                                                                  GACGGCAATACATCCACGTGCTGGACCCCAGTGACACTACAGTGGCAGTCAAGTACGTC
                                                                                                               220 CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGT
proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of HCV infection.
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus, HCV, non-A non-B, envelope 1 gene; isolate S52, diagnosis; vaccines; antibodies; antisera; gene inhibition; ss.
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                                                           Query Match 60.9%; Score 383.6; DB 17; Length 576; Best Local Similarity 96.6%; Pred. No. 6.9e-113; Anatches 392; Conservative 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                               CATCTTTCAGGACATCGAATGCCTTGGGATATGATGATGATTGGT 406
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                                         Sequence 576 BP; 110 A; 156 C; 163 G; 147 T; 0 other;
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P-PSDB; AAR69671.
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19-SEP-1995
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                                                                                                                                                                                     280 ATTGTGTACGAGGCCGATGACGTTATTCTGCACACCCCGGCTGCATACCTTGTGTCCAG
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/product= envelope-1_protein
/note= "does not contain start or stop codon"
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Query Match
60.6%; Score 382; DB 16;
Best Local Similarity 96.3%; Pred. No. 2.3e-112;
Matches 391; Conservative 0; Mismatches 15;
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181 GGAGCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTGGTGGGGCGCGGCCACTATG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ81881 encodes AAR69670 hepatitis C virus (HCV) envelope 1 (E1) protein isolate S2, both can be used for the diagnosis of HCV infection, and in the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may also be used to inhibit the expression of the HCV E1 game.
 Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate S2; diagnosis; vaccines; antibodies; antisera; gene inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                      Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-nucleotide(s), peptide(s) and proteins, used in diagnosis and in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 576;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.4%; Score 380.4; DB 16; Length Best Local Similarity 96.1%; Pred. No. 7.4e-112; Matches 390; Conservative 0; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Updated on 25-MAR-2003 to correct PN field.)
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                                                                      Location/Qualifiers
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P-PSDB; AAR69670.
                                                                                                                                                                                                                                                                                Miller RH,
                                            Hepatitis C virus.
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                                                                                                                                                                                                                                                            AAT16559-T16609 are cDNAs encoding the El (envelope-1) protein of 51 H isolates. The isolated sequences are useful for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of HCV infection.
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1 to determine HCV genotype and as vaccines against HCV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 382; DB 17;
Pred. No. 2.3e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                      DEPT HEALTH & HUMAN SERVICES SEC DEPT HEALTH.
                                                                                                                                                                                                                                    Claim 1; Page 101-102; 340pp; English.
                                                                                                                  Bukh J, Miller RH, Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                                                                              60.6%;
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               95WO-US10398
                                            94US-0290665
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P-PSDB; AAR89542.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)

Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Gu,J., Zin,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Li,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z.
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Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanz@chgog.ch.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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                                                                  BE428299
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Total number Minimum DB Maximum DB

Database

Š. Result

Searched:

Sequence:

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by relocity. The sheared DNA 0.05 inch orifice at constent velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were
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2M0275007R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0275007 R, genomic survey sequence.
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Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/lab host="E. coli strain XL10-Gold, Tl-resistant, F-"
/lab host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PW942nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jacks
Laboratory Mouse DNA Regource,
                                                                                                                                                                                                                          481 ACATÁGTIGIGCATACACATGCIGIGATCAGCICACTÁCGIGITGGACCICTGCGITG
                                                                                                                                                                                                                                                                                                   494 CTGTCTTCCTCGTGGGACAAGCCTTCACGTTCAGACCTCGTCGCCATCAAACGGTCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             554 CCTGTAACTGCTCGCTGTACCCCAGGCCATCTTTCAGGAC-ATCGAATGGCTTGGGATATG
                                                                                                                                             434 ACCTATTAGTGGGCGCGCGCGCACGATGTGCTCTGCGCTCTACGTGGGTGACATGTGTGGGG
Length 492;
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Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: 0 column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 633.
Iocation/Qualifiers
        Score 40.2; DF
Pred. No. 8.1;
        Query Match
6.4%; Score 40.2; D
Best Local Similarity 57.5%; Pred. No. 8.1;
Matches 111; Conservative 0; Mismatches
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/60"
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/clone="UUGC2M0275007"
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Fax: 801 585 7177
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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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AV758366 BM Homo sapiens cDNA clone BMFAKA03 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 CAACTGCTCCATCTATCCTGGGGCCATCACTGGACACGTATGAGCATGGGGAATGATGATGA 300
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/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="BM"
/note="Vector: priplEx2; Site_1: sfiIA; Site_2: sfiIB"
/note="Vector: priplEx2; Site_1: sfiIA; Site_2: sfiIB"
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Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
315 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                  /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="BM2": pTriplEx2; Site_1: sfilA; Site_2: sfilB"
/note="Vector: pTriplEx2; Site_1 4 others
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8.5%; Score 53.8; DB 9; Length 488;
Best Local Similarity 62.4%; Pred. No. 0.0026;
Matches 118; Conservative 0; Mismatches 67; Indels 4
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/organiam="Homo sapiens"
/mol_type="mkNA"
/db_xref="taxon:9606"
/clone="BMFAKA03"
                1. .488
/organism≃"Homo sapiens"
                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BMFAKB03"
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ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 k range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10.Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
1 (bases I to 521)
2 (Bases I to 521)
3 (Bases I. O. Grose, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, B., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross match with the -minscore 18 and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 ATTTGCCCGGTTGCTCCTTTTCTATTTTCCTTCTCGCTCTGTTCTTCTTAATTCATC 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 TAGTACCTAGACTAGAAAGCTATAAACTTTTGTGGAGTATGATCTTAGCACAGCCCTTT 563
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                      89 CAAGAGCCCTTGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAATTTCGCAACAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 GCATCACCGGTTAGAGATCATCTGGTTTAGTTTTCCCTGCTGGGTCTACACTCATTTTTC
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                                                                                                                                                                                                                                                                                                    Length 633;
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                  Score 40.2; DB 28;
Pred. No. 8.4;
0; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACKWARD: GTTTTCCCAGTCACGACG
Plate: S8 row: J column: 15
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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BE756035.1 GI:10170027
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l Similarity 51.4%;
93; Conservative (
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BW161485 Nori Satch unpublished cDNA linear EST 03-NOV-2002 BW161485 Nori Satch unpublished cDNA library, gonad Ciona intestinalis cDNA clone rcigd042005 3', mRNA sequence.
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Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 cigecinica redicione a caractración de contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra c
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                                                                                                                                                                                                                                                                               /notes="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sall; Library made from pooled tissue From testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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a 97 c 117 g 102 t 5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 CGTGCGGATTCGCCGATCTCATGGGGTACATCCCGCTCGTCGCGCGCTCCCCGTAGGAGGCG
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1 (bases 1 to 423)
1 Stou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
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llarity 47.4%; Pred. No. 33;
Conservative 0; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: satoh@ascidian.zool.kyoto~u.ac.jp
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.1%; Score 38.4; Di
51.1%; Pred. No. 24;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           adrenal, and endometrium."
          taurus"
                                                                                                                                                                                                                                               lib="MARC 2BOV"
                                                    /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                        db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
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organism="Bos
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Contact: Nori Satoh
Department of Zoology
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                                                                                                                                                                                                                                          /clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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/ Lew LOUSE = JULIANDE MGC 116"
//clone lib="NIH MGC 116"
//note="Organ: pooled colon, kidney, stomach; Vector:
//note="Organ: pooled colon, kite_2: EcoRV (destroyed); RNA pCMV-SPORT6: Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of chemale, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is oligo-dT primed and directionally cloned (EcoRV site is distributed). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE428299 MENA linear EST 26-JUL-2000 MTD005.E02F990616 ITEC MTD Durum Wheat Root Library Triticum turgidum subsp. durum cDNA clone MTD005.E02, mRNA sequence. BE428299 GI:9426142 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 CACCIACAGICACAGICAAGIACGICGGAGCAACCACGGCITCGAIACGCAGICAIGIGG 433
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                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMI1404 row: k column: 14
High quality sequence stop: 524.
High quality sequence stop: 524.
                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1252)

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                                                                                                                                                      NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.9%; Score 37.4; Diguery Match
Best Local Similarity 49.7%; Pred. No. 48;
Matches 95; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
/clone="tMAGE:5163013"
/lab_host="tDH108"
           BIS17398.1 GI:15342190
                                                        Homo sapiens (human)
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                VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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ACCESSION
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1 (bases 1 to 701)

Satou Y., Shin-i,T., Kohara,Y. and Satoh,N.

Expressed genes in Ciona intestinalis (2002c)
                                            251 acitecratragreadecerridedececarerraararreecedderredecadaraceeddag 192
  352 TCCACGTGCTGGACCCCAGTGACACCTACAGTGGCAGTCAAGTACGTCGGAGCAACCACC 411
                                                                                         GCTTCGATACGCAGTCATGTGGACCTATTAGTGGCGCGGCCACGATGTGCTCTGCGCTC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Ciona intestinalis"
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/tissue type="gonad"
/clone lib="Nori Satoh unpublished cDNA library, gonad"
166 c 185 g 165 t 3 others
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Pred. No. 35;
0; Mismatches 109;
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Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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Department of Zoology
Kyoto University
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                                                      Eukaryota; Viridiplantes; Etreptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticae; Triticum.

1. Triticae; Triticum.

2. Triticae; Triticum.

3. Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier, S., Dubcovsky,J., Foullie,C., Gale,M., Graher,A., Guberafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Olai,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pacchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.

International Triticaea EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae

Unpublished (2000)

Contact: Joudrier P

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Tel: 33 4 99 61 23 48
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Populus tremula x Populus tremuloides
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
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/dev_stage="3-day-old seedling, water-stressed"
/clone_lib="lTTEC MTD Durum Wheat Root Library"
/note="Vector: pSPORT1; T7 primers used. See pSPORT1
polylinker site. 0.3-2.0 KDp average insert size."
66 c 148 g 74 t 6 others
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/mol_type="mRNA"
/cultivar="Siliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bmail: joudrier@ensam.inra.fr
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
Triticum turgidum subsp. durum (durum wheat)
Triticum turgidum subsp. durum
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Pred. No. 53;
0; Mismatches 95,
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/clone="MTD005.E02"
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Populus tremuloides (quaking aspen)
Populus tremuloides
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, rosids
, eurosids I, Malpighiales; Salicaceae; Populus.
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Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished
Contact: BHALERAO RUPALI R.
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 5676
Email: rupal: halerao@plantphys.umu.se.
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Plant Biotech Research Center
Michigan Technological University, School of Forest Resources
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
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/mol_type="mRNA"
/db_xref="taxon:47664"
/tisme_type="imbibed seed"
/clone_lib="Populus imbibed seed cDNA library"
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/mol_type="mRNA"
/db_xref="texon:3693"
/clone_lib="Aspen leaf cDNA Libra
/note="Organ: leaf"
a 162 c 101 g 97 t
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Pred. No. 59;
0; Mismatches
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MTUTI.P12.F05 Aspen leaf cDNA Library Populus tremuloides cDNA,
mRNA sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
eurosids I; Malpighiales, Salicaceae, Populus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
Contact: Tsai C-J
Contact: Tsai C-J
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Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2914
Email: chtsai@mtu.edu.
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Length 544;
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50.6%; Pred. No. 62;
cive 0; Mismatches 87; Indels
Score 36.8; DB 14; Length
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0; Mismatches 87; Indels
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/mol_type="manAn"
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/note="Organ: leaf"
/note="Organ: leaf"
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Location/Qualifiers
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/organism="Populus tremuloides"
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Populus tremuloides (quaking aspen)
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RESULT 12 CA924833/c

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Populus tremuloides (quaking aspen)
Populus tremuloides
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.

(bases 1 to 577)
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MTU7CL.P4.D04 Aspen leaf cDNA Library Populus tremuloides cDNA,
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1 (bases 1 to 569)
Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and Tsai
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CA924833 SET 27-DEC-2002 MRNA linear EST 27-DEC-2002 MTUTEL.P10.B12 Aspen leaf cDNA Library Populus tremuloides cDNA,
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Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
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Michigan Technological University, School of Forest Resources
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Latin Townsend Drive, Houghton, MI 49931-1295, USA
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
Location/Qualifiers
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/db_xref="taxon:3693"
/dlone_lib="Aspen leaf cDNA Library"
/note="Organ: leaf"
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50.6%; Pred. No. 62;
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Best Local Similarity 50.6°
Matches 89; Conservative
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Populus balsamifera subsp. trichocarpa
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 578) Therefore and Sterky. F.
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/note="Organ: flower"
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Pred. No. 62;
0; Mismatches 87; Indels
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                                                                           1. 577

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/mol_type="maxon:3693"

/db xref="taxon:3693"

/clone_lib="Aspen leaf cDNA Library"

/note="Organ: leaf"

/note="Organ: leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
Inversity of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
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Location/Qualifiers
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1400 Townsend Drive, Houghton,
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
Location/Qualifiers
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Matches 89; Conservative
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Matches 89; Conservative
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TITLE
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BU881720
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BW153281

BW153281 Nori Satoh unpublished cDNA library, gonad Ciona intestinalis cDNA clone rcigd020b10 3', mRNA sequence.
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1 (Dases 1 to 465)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
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                                 141 CCCAAAGACGCTGGCCTCAATGACCAAAAGAACTTCATCGCATATGGCGGTGTAGGTGGC 200
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| 109 c 123 g 111 t lothers
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229 CGGAATACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTAC
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Pred. No. 68;
0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Zoology
Kyoto University
Sakyoto, Wyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Ciona intestinalis"
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Matches 102; Conservative
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Sequence 29, Application US/08612973

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| CORRESPONDENCE ADDRESS: |
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| ADDRESSEE: ALONGY WANDERHYE P.C. |
| CONFUTENT INFORMATION |
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| APPLICATION NUMBER: 13,205 |
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               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 1008
Listing first 45 summaries
                                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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241 GGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGCCGATGAC 300
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                                  Version #1.25 (EPO)
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Best Local Similarity 100.0%; Pred. No. 1.4e-200;
Matches 630; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                            ALIGNATION NUMBER: 32,205
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REFRENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SOFTWARE: PATENTIN RC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/927,597
                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
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ANTI-SENSE: NO
FEATURE:
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FEATURE:
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APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUXSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
CORRESPONDENCE: 111
CORRESPONDENCE ADDRESS:
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                                                                    Length 630;
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                                                                        100.0%; Score 630; DB 3; L
100.0%; Pred. No. 1.4e-200;
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STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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Best Local Similarity 100.
Matches 630; Conservative
                                      US-08-612-973-29
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       460 TGCTCTGCGCTCTACGTGGGTGACATGTGGGGGCTGTCTTCCTCGTGGGACAAGCCTTC
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DIAGNOSTIC METHODS AND VACCINES
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Pred. No. 2.9e-118;
0; Mismatches 14;
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APPLICANT: BUCH, J., MILLER, R.H. AND
TITLE OF INVENTION: AMINO ACID SEQUENCES
TITLE OF INVENTION: OF 51 ISOLATES OF HE
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TITLE OF INVENTION: OF RAGENTS DERIVED
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TITLE OF INVENTION: DIAGNOSTIC METHODS AND MERGEN OF SEQUENCES: 159
CORRESPONDENCE ADDRESS: 159
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-UUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION ATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-UUN-1993
CLASSIFICATION: 24
ATTORNEY/AGENT INPORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39, Application US/08468570 Patent No. 5871962
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REFERENCE/DOCKET NUMBER: 202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
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Best Local Similarity 96.6%;
Matches 392; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INDIVIDUAL ISOLATE: S
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MEDIUM TYPE: FLOPPY
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COUNTRY:
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                                                               541 CAAACGGICCAGACCIGIAACIGCICGCIGIACCCAGGCCAICITICAGGACAICGAAIG 600
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US-08-086-428B-39
i Sequence 39, Application US/08086428B
j Sequence 39, Application US/08086428B
j Patent No. 5514539
i GENERAL INFORMATION:
    APPLICANT: BUKH, J., MILLER, R.H. AND
    APPLICANT: BUKH, J., MILLER, R.H.
    TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
    TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE I GENE
    TITLE OF INVENTION: OF SEAGENTS DERIVED FROM THESE SEQUENCES IT ITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN NUMBER OF SEQUENCES: 159
    CORRESPONDENCE ADDRESS: 159
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                        601 GCTTGGGATATGATGATGAACTGGTAATAG 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPREFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08 086, 428B
FILLING DATE: 29-JUN-1993
CLASSIFICATION: 435
ATORNEY AGENT INFORMATION:
NAME: RICHARD W BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEFHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 576 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 345 PARK AVENUE
NEW YORK
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-086-428B-39
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APPLICANT: BUKH, J., MILLER, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF REAGENTS OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES INTILE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES INTILE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                    220 CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGT
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                                                                       Score 383.6; DB 2;
Pred. No. 2.9e-118;
                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,601A
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
PRICH APPLICATION DATA:
APPLICATION NUMBER: 29-JUN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-466-601A-39
; Sequence 39, Application US/08466601A
; Patent No. 6572864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLOPPY DISK
                                                                             Query Match 60.9%;
Best Local Similarity 96.6%;
Matches 392; Conservative
) ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: S54
US-08-290-665A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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                                                                                   280 ATTGTGTAACGAGGCCGATGACGTTATTCTGCACACCCGGCTGCATACCTTGTGTCCAG 339
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                                           CTAGAGTGGCGGAATACGTCTGGCCTCTATATCCTTACCAACGACTGTTCCAATAGCAGT 60
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APPLICANT: BUXH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                       GGAGCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGCCGCCACGATG
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      CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGT
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: 1BM PC COMPATIBLE
COMPUTER: 1BM PC COMPATIBLE
COMPUTER: 1BM PC-DOS/MS-DOS
SOFTWARE: WONDERFERCT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORNK
REGISTRATION NUMBER: 36,459
REPERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-08-290-665A-39
US-08-290-665A-39
Sequence 39, Application US/08290665A
Patent No. 5882852
Patent INFORMATION:
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INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 576 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
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Pred. No. 2.9e-118;
0; Mismatches 14;
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Patent No. 5514539
GENERAL INFORMATION:
APPLICANT: BUKKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
                        PCT/US95/10398
                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 UUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                            NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFRENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                     39;
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                                                                                                                                                                                                                                                                                                                               TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.9
Best Local Similarity 96.6
Matches 392; Conservative
                          APPLICATION NUMBER: FILING DATE: 15-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: PURCELL,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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TOPOLOGY: lir
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                                                                                                           Score 383.6; DB 4; Length 576;
Pred. No. 2.9e-118;
0; Mismatches 14; Indels 0
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                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF SEQUENCES
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TITLE OF SEQUENCES
CORRESPONDENCE ADDRESS:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
REFERENCE/DOCKET NUMBER: 2026-4070USZ
ELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 756-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: WORDPERPECT 5.1
                                                                      INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 576 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                           60.9%;
                                                                                                                                                                                      TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: homosapiens
iNULVIDUAL ISOLATE: S54
US-08-466-601A-39
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                                                                                                                                                                                                                                                                                                       Query Match 60.9
Best Local Similarity 96.6
Matches 392; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
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                                                                 Gaps
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NUCLECTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
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Length 576;
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NUCLECTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEAPITITE C AND THE USE
OF REAGENTS DERIVED FROW THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: ENABLE FLORPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION NUMBER: 36,428
ATTORNEY/AGRAT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: (212) 751-6849
                                                 MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                              ADDRESSER: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                       APPLICANT: BUKH, J., MIL
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCI
TITLE OF INVENTION: OF 5
TITLE OF INVENTION: OF 5
TITLE OF INVENTION: OF 7
TITLE OF INVENTION: DIAG
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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60.6%; Score 382; DB 1; Length 576;
Best Local Similarity 96.3%; Pred. No. 1e-117;
Matches 391; Conservative 0; Mismatches 15; Indels
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                     COUNTY: USA

ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDBERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,428B
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELEPHONE: (212) 758-480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 421792
INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS: LENGTH: 576 base pairs TYPE: nucleic acid STRANDEDNESS: single STRANDEDNESS: single TOPOLOGY: linear ORIGINAL SOURCE: ORIGINAL SOURCE: SCANISM: homosapiens INDIVIDUAL ISOLATE: S52 US-086-428B-38
                                                                                                                                                                         CITY: NEW
STATE: NI
COUNTRY:
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60.6%; Score 382; DB 2; Length 57
Best Local Similarity 96.3%; Pred. No. 1e-117;
Matches 391; Conservative 0; Mismatches 15; Indels

RESULT 9 US-08-468-570-38 ; Sequence 38, Application US/08468570

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520 ACGITICAGACCITCGICGATCAAACGGICCAGACCIGIAACTGCICGTCGCTGTACCCAGGC 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKELL, R.H.
APPLICANT: BUKELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSES: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STARTE: NEW YORK
STARTE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                          220 CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGT
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                                                                                                                                                                                                                                             Query Match 60.6%; Score 382; DB 5; Length 576; Best Local Similarity 96.3%; Pred. No. 1e-117; Matches 391; Conservative 0; Mismatches 15; Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,428B
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 37, Application US/08086428B; Patent No. 5514539
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                                                                                                                                             ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S52
PCT-US95-10398-38
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
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PCT-US95-10398-38

Sequence 38, Application PC/TUS9510398

GENERAL INFORMATION:
MULLER, R.H. AND
APPLICANT:
PURCELL, R.H.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
SEQUENCES OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION:
SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE:
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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                    CTAGAGTGGCGGAATACGTCTGGCCTCTATGCCAACGACTGTTCCAATAGCAGT
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ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
PILING DATE: 15-AUG-1995
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REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 758-4800
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION NUMBER: 08/290/665
APPLICATION NUMBER: 08/290/665
APTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 421792
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
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121 GACGGTAATACATCCACGTGGACCCCAGTGACACCTACAGTGGCAGTCAGGGTATGTC 180
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NUCLECTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HERATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
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Pred. No. 3.4e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                         ADPLICATION NUMBER: US/08/468,570
FILING DATE: 6-JUN-1995
CLASSIPTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIPTCATION: 424
ATTORNEY/AGENT INCRWATION:
NAME: RICHARD W. BORK
REGISTATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MILLER, R.H. AND
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Patent No. 582825
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AN APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: AMINO ACID SEQUIPATION OF TITLE OF INVENTION: CORE GENES OF ITLE OF INVENTION: AND THE USE OF ITLILE OF INVENTION: AND THE USE OF ITLILE OF INVENTION: AND THE USE OF ITLILE OF INVENTION: AND THE USE OF IT
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INDORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
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Best Local Similarity 96.1%;
Matches 390; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
                                                            CURRENT APPLICATION DATA:
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INDIVIDUAL ISOLATE: S:
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TOPOLOGY: lir
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US-08-290-665A-37
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OF 51 ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 380.4; DB 1; Length 576;
Pred. No. 3.4e-117;
0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 CAICTTTCAGGACATCGCATGGCTTGGGATATGATGATGATTGGT 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BURH, J., MILLER, R.H. AND APPLICANT: BURH, J., MILLER, R.H.
TITLE OF INVENTION: UNCLECTIDE AND DEDUCED TITLE OF INVENTION: AMINO ACID SEQUENCES OF TITLE OF INVENTION: OF S1 ISOLATES OF HEPATITITLE OF INVENTION: OF REAGENTS DERIVED FROM TITLE OF INVENTION: DIAGNOSTIC METHODS AND VAN NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FINNEGAN
                                                                                                                              TELEX: 421792
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 96.1%;
Matches 390; Conservative
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                                                                                                                                                                                                                                                                                                                                   ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S2
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MEDIUM TYPE: FLOPPY
COMPUTER: IBM PC COM
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US-08-468-570-37
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1 CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCCTCACGACGACTGTTCCAATAGCAGT
IIILE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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Pred. No. 3.4e-117;
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ZIP: 10154

ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATE:
APPLICATION MANE: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION NUMBER: 2026-4116
ATTORNS/FICATION NUMBER: 2026-4116
REGISTRATION NUMBER: 2026-4116
REFERENCE/DOCKET NUMBER: 2026-4116
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STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
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December 19, 2003, 16:55:48; Search time 2385.36 Seconds (without alignments) 10804.703 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | 7341 Semience | AXAE2780 Seguence | 0 0 | Sequent | ¢ | t apriants | AX03162/ Sequence | AX031897 Sequence | Sequence | BD172148 New seque | A40653 Sequence 53 | AX031631 Sequence | AX031901 Sequence | AX032171 Sequence | BD172150 New seque | A40651 Seguence 51 | AX031629 Seguence | AX031899 Sequence | AX032169 Sequence | BD172149 New Secure | A40645 Semience 45 | . A40647 Semience 47 | AX031623 Sequence | AX031625 Segmence | AX031893 Sequence | AX031895 Seguence | AX032163 Sequence | AX032165 Segmence | BD172146 New secue | BD172147 New Recine | A40753 Semience 15 | AX031731 Sequence | AX032001 Semience | AX032271 Semience | AD172193 New Section | 1.29582 Henatitis C | DS0466 Henatitis C | 1 1 | 44 Henatit | emience 1 | A40795 Seminary 19 | d Chairman | | Semienc | AX032043 Sequence | | | É | inear PAT 0/-MAK-199/ | | • | | | | S | NS FOR DIAGNOSTIC AND | | |
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| 03 | | | | | _ | ۳ | | | | | | | | | | | | | | | | | | | | | | | | | | | · w | | | | 4 | 4 | 14 | 14 | | | | | | 9 | | | | Patent | 3 | 406 | | | | | | 4 | \$ |
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| Ŏ. | | 630 | 9 6 | 000 | 200 | 100 | 7 00 | 200 | 909 | 209 | 602 | 6009 | 600.8 | 600.8 | 600.8 | 6009 | 597.2 | 597.2 | 597.2 | 597.2 | 597.2 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 73 | 573.2 | 73 | 7 | 3.5 | S. | 539.6 | | . 4 | 0 | 12 | , , | 2 | 10 | 510.2 | | 1 | | | | | | | | | | | _ |
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Location/Qualifiers
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic
therapeutic use
Patent: US 6245503-A 31 12-JUN-2001;
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Best Local Similarity 100.0%; Pred. No. 1.96-170;
Matches 630; Conservative 0; Mismatches 0;
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AX452780
      630 bp i Sequence 31 from patent US 6245503.
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171 c 170 g
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AR157341.1 GI:16218275
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NYATGNLPGCSFSIFILALLSCLTVPASAVPYRNASGIYHVTNDCPNSSIVYEADNLI
LHAPGCVPCVMTGNVSRCWVQITPTLSAPSLGAVTAPLRRAVDYLAGGAALCSALYVG
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Mustied Hepatitis C Virus envelope proteins for diagnostic therapeutic use
Patent: WO 02055548-A 31 18-JUL-2002;
INNOGENETICS N.V. (BE)
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Hepatitis C virus
Viruses: ssRNA positive-strand viruses,
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DACGALFLVGQMFTYRPRQHATVQNCNCSIYSGHVTGHRMAMDMMNW"
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Hepatitis C virus
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Hepacivirus.
                                                                                                                                                                                                                                   virus"
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Maertens, G. and Stuyver, L.
NEW SEQUENCES OF HEPAITIS C VIRUS GENOTYPES AND THEIR THERAPEUTIC AND DIAGNOSTIC AGENTS
PATENT: WO 9425601-A 49 10-NOV-1994;
INNOGENETICS NV (BE)
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                            Length
                            95.6%; Score 602; DB 14; L
100.0%; Pred. No. 2.3e-162;
ive 0; Mismatches 0;
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LJILAPGCCVPCVMTGWVSRCWVQITPTLSAPSLGAVTAPLRRAVDYLAGGAALCSALY
VGDACGALFLVGGALFYRRQHATVQNCNCSIYSGHVTGHRMA"

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Best Local Similarity 100.0%; Pred. No. 2.3e-162;
Matches 602; Conservative 0; Mismatches 0;
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therapeutic and diagnostic agents
Patent: EP 1004670-A 49 31-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                             /proteIn_id="CAC09689.1"
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Location/Qualifiers
1. 959
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Sequences of hepatitis
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LILHARGCVPCVWTGNVSRCWVQITPTLSAPSLGAVTAPLRRAVDYLAGGAALCSALY
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95.6%; Score 602; DB 6; Le
Best Local Similarity 1100.0%; Pred. No. 2.3e-162;
Matches 602; Conservative 0; Mismatches 0;
                                                                                                    3. . > 959
/note="unnamed protein product"
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Sequence 49 from Patent EP1004670.
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Location/Qualifiers
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LOUDACGALFLVGGARTYRRQHATVQNCNCSIYSGHVTGHRNA"
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ACGCGTGTGGGGGCACTATTCTTGGTAGGCCAAATGTTCACCTATAGGCCTCGCCAGCACG
                                                                                                                                                                      GGAGAGCCGTTGACTACCTAGCGGGAGGGGCTGCCCCTCTGCTCGGCGTTATACGTAGGAG
                                                                                                                        ACGCGTGTGGGGGCACTATTCTTGGTAGGCCAAATGTTCACCTATAGGCCTCGCCAGCACG
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100.0%; Pred. No. 2.3e-162;
iive 0; Mismatches 0;
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/note="unnamed protein product"
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Sequence 49 from Patent BP0984067.
AX032167
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lillapagcvycvymtgvsrcwvjitpilsabelgavypslrrandprsslvysadn
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al Similarity 100.0%; Pred. No. 2.3e-162;
602; Conservative 0; Mismatches 0;
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/note="unnamed protein product"
/codon start=1
/protein id="CAC09766.1"
/db_xref="GI:10279048"
                                                                                                                                                          DNA
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Sequence 49 from Patent EP0984068.
AX031897.1 GI:10279047
                                                                                                                                                                                                                                                                                                                                                                                    /organism="unidentified"
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/db_xref="taxon:32644"
/clone="PC-3-4"
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Maertens,G. and Stuyver,L.
Mertens,G. and Stuyver,L.
NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS THERAPECTIC AND DIAGNOSTIC AGENTS
PATENT: WO 9425601-A 53 10-NOV-1994;
INNOGENETICS NV (BE)
Other publication CA 2139100 941121
Other publication CN 1108030 950906
Other publication CN 1108030 950906
Other publication FI 946066 941223
Other publication NO 944967 941221
Other publication JP 7508423T 950921.
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JP 2002233389-A/25
20-AUG-2002
21-NOV-2001 JP 2001356707
27-APR-1993 EP 93402019.9 PI
T MAERTENS, LIEVEN STUYVER
GIZNIS/09, AGIK35/76, AGIK38/00, AGIK39/00, AGIK39/395, AGIK39/00, AGIK48/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK39/00, AGIK3
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New sequences of hepatitis C virus genotypes for diagnosis,
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GGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCAGATAACC
                                                                                        658 TGATCCTACACGCACCTGGTTGCCTGCCTTGTGTCATGACAGGTAATGTGAGTAGATGCT
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ORS Macrens, G. and Stuyver, L.

New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy

AL Patent: JP 2002233389-A 25 20-AUG-2002;

NV INNOGENETICS SA

OS Unidentified

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New sequences of hepatitis C virus genotypes for
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JP 2002233389-A/25.
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al Similarity 99.5%; Pred. No. 5.1e-162; 599; Conservative 3; Mismatches 0;
                                                                                                                                                                                                                    /note="unnamed protein product"
                                                                                     Sequences of hepatitis c virus genot
therapeutic and diagnostic agents
Patent: EP 1004670-A 53 31-MAY-2000;
INNOGENETICS NV (BE)
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VGDACGALPLVGGWRTYRPRQHATVQNCNCSIYSGHVTGHRMA"

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Sequence 53 from Patent BP1004670.
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                                                                                                                                                                                                                                              418 TCGTAGGCGGCCCCRTTGGGGGGCGTCGCAAGGCTCTCGCACACGGTGTGAGGGTCCTTG
    778 GGAGAGCCGTTGACTACCTAGCGGGGGGGCTGCCCTCTGCTCCGCGTTATACCTAGGAG
                                                                                                                                                           482 ACGCGTGTGGGGCACTATTCTTGGTAGGCCAATGTTCACCTATAGGCCTCGCCAGCACG
                                                                                                                                                                                      838 ACGCGTGTGGGGCACTATTCTTGGTAGGCCAAATGTTCACCTATAGGCCTCGCCAGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 TGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTAYATCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 TOGTAGGCGGCCCCATTGGGGGCGTCGCAAGGGCTCTCGCACGCTGTGAGGGTCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 AGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTTTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478 AGGACGGGGTAAACTATSCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTTATTC
                                                                       GGAGAGCCGTTGACTACCTAGCGGGGGGGCTGCCCTCTGCTCCGCGTTATACGTAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTATATCCCGC
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Patent: EP 0984067-A 53 08-MAR-2000;
INNOGENETICS NV (BE)
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    >959
    /note="unnamed protein product"

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1. 959
Acganism="unidentified"
| forganism="unidentified"
| do xref="texon:32644"
| clone="PC C/51"
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Matches 59
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
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VERSION
KEYWORDS
SOURCE
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TITLE
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AX032171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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SRPNWGPNDPRRKSRNLGKVIDTLTCGFADLMGYIPLVGGPXGGVARALAHGVRVLED
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LILHAPGCVPCVMTGNVSRCWVQITPTLSAPSIGAVTAPLRRAUDXLAGGAALCSALY
VGDACGALFLVGQMFTYRPRQHATVQNCNCSIYSGHVTGHRMA"
285 C 13 others
                                                                                                                                                                                                                            PAT 20-SEP-2000
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                           957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGTAGGCGCCCCATTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTCCTTG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGTAGGCGCCCCRTTGGGGGCGTCGCAAGGCTCTCGCACACGGGTGTGAGGGGTCCTTG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATTTTTTTC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCAGATAACC 657
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TGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTATATCCCGC
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Pred. No. 5.1e-162;
3; Mismatches 0;
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                                                                                                                                                                                                                            DNA
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therapeutic and diagnostic agents
Patent: EP 0984068-A 53 08-MAR-2000;
INNOGENETICS NV (BE)
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Corganism="unidentified"
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/clone="PC C/E1"
                                                                                                                                                                                                                            959 bp
EP0984068
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GGAGAGCCGTTGACTACCTAGCGGAGGGGCTGCCCTCTGCTCCGCGTTATACGTAGGAG 481
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                                                                                                                                                                                                                                       TGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCATGACAGGTAATGTGAGTAGATGCT
                                                                                                                                                                                                                                                                               TIGCICITCICICGGIGICICIGACCGTICCGGCCTCTGCAGTICCCTACCGAAAIGCCTCTG
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                                                                                                            TGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTATATCCCCGC
                                                                   Length 959;
                                     Indels
               Score 600.8; DB 6;
Pred. No. 5.1e-162;
3; Mismatches 0;
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                Query Match
Best Local Similarity 99.5%;
Matches 599; Conservative
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1 (bases 1 to 959)

Martens, G. and Stuyver, L.

Revences of hepatitis C virus genotypes for diagnosis,

Prophylaxis and therapy

NAL PP 2002233389-A 27 20-AUG-2002;

NV INNOGENETICS SA

OS Unidentified

PR 2002233389-A/27

PD 20-AUG-2001

PP 21-NOV-2001 JP 2001356707

PP 21-NOV-2001 JP 2001356707

PR 27-APR-1993 EP 93401099.2, 05-AUG-1993 EP 93402019.9 PI

GREKT MARKTENS, LIEVEN STUYVER

PC CLINIS, O9, A61K48/O0,

PC A61K48/O0,

PC A61K48/O0,

PC A61K48/O0,

PC A61K48/O0,
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                                GGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCAGATAACC 301
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Strandedness: Single;
Topology: Linear;
New sequences of hepatitis C virus genotypes for diagnosis,
prophylaxis
                                                                                     GGGTCCAAATTACCCCTACACTGTCAGCCCCCAGCCTCGGAGCAGTCACGGCTCCTCTTC
                                                                                                                                                              GGAGAGCCGITGACTACCTAGCGGGAGGGGCTGCCCTCTGCTCCGCGTTATACGTAGGAG
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                                                                                                                                                                                                                  TGATCCTACACGCACCTGGTTGCGTGCCTTGTGACAGGTAATGTGAGTAGATGCT
                                             959 bp DNA linear PAT 18-New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy.
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/organism="genomic DNA"
/db_xref="taxon:32644"
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BD172150.1 GI:28413448
JP 2002233389-A/27.
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1 ATGGTAAGGTCATCGATAC.....TGATGATGAACTGGTAATAG
version 5.1.6
- 2003 Compugen Ltd.
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Listing first 45 summaries
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      GenCore (c) 1993
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AAQ43889
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AAT12966
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1 and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the conversion in the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage, or a reduction step with a carrying out a disulphide bond cleavage agent, after 1945 of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or constructs can also be immobilised on a solid substrate and incorporated constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or into a reversed phase hybridisation assay for determining the presence or che genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and conformation expressed E1, E2 and E1/E2, and are more reactive with human sera than those isolated by known
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proteins - in presence of di:sulphide bond cleavage agent, to
produce proteins suitable for direct use in vaccines or diagnostic
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are against HCV. The recombinant HCV B1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTIGCTCTTCTCTCGTGTCTGACCGTTCCGGCCTCTGCAGTTCCCTACCGAAATGCCTCT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGACGGGGTAAACTATGCGAACAGGGAATTTAACCCGGTTGCTCTTTCTCTTTATT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New therapeutic vaccine compositions comprising at least one purifit recombinant hepatitis C virus (HCV) single or specific oligometic recombinant envelope protein El or E2, useful for immunizing humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                   E2 protein; infection; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 630; DB 24; Length 630; 100.0%; Pred. No. 2.9e-186; Indels 0; Mismatches 0; Indels 0
                                                                                                                                                                        Hepatitis C virus clone HCCI63 E1 protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 630 BP; 126 A; 171 C; 170 G; 163 T; 0 other;
601 GCATGGGATATGATGATGAACTGGTAATAG 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 184-185; 243pp; English.
                                                                                                                                                                                                          Hepatitis C virus; HCV; El protein;
virucide; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buyse
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30-AUG-2001; 2001US-315768P.
                                                                                                                                                                                                                                                                                                                                                          11-JAN-2002; 2002WO-EP00219.
                                                                                   630
                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (INNO-) INNOGENETICS NV
                                                                                 AAL48930 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bosman F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-599657/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Begt Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    From HCV infection
                                                                                                                                                                                                                                                                Hepatitis C virus.
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                                                                                                                                                                                                                                                                                             WO200255548-A2.
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                                                                                                                                                  24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maertens G,
                                                                                                                                                                                                                                                                                                                             18-JUL-2002.
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                                                                                                                   AAL48930;
                                                                       AAL48930
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Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more particularly (i) the region spanning positions 417-57 of the Core/El region of HCV subtype 3a; (ii) the region spanning positions 464-4730 of the NS3 region of HCV type 3; (iii) the region spanning positions 4892-292 of the NS3 region of HCV type 3; (iii) the segion spanning positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype 3a; or (v) an HCV subtype 3c genomic sequence, or from a subtype 2d sequence, a type 4 genomic sequence, or the coding region of subtype 5a, may be used as primers to amplify nucleic acid from an isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid. Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the compositions may be used for immunisation against HCV, for the compositions may be used for immunisation against HCV, for the compositions may be used for immunisation of a secotyping. This sequence corresponds to the El region of HCV subtype 5a and is taken from a clone designated PC-3-4.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       838 ACGCGTGTGGGGCACTATTCTTGGTAGGCCAAATGTTCACCTATAGGCCTCGCCAGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         898 CTACGGTGCAGAACTGCTACCATTTACAGTGGCCATGTTACGGCCACGGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 TGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTATATCCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538 TIGCTCTTCTCTCTGTGTCTGACGTTCCGGCCTCTGCAGTTCCCTACCGAAATGCCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 GGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCAGATAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      718 GGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCACGGCTCCTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 GGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCACGGCTCCTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 959 BP; 189 A; 285 C; 270 G; 215 T; 0 other;
      Claim 3; Page 138-139; 404pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
nes 602; Conservative
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GGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCAGATAAC
                                                                                          GGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCAGATAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; primer; probe; detection; diagnosis; classification; immunisation; prophylaxis; serotyping; ss.
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93EP-0402019
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(first entry)
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05-AUG-1993;
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02-AUG-1995
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118 TCGTAGGCGCCCCRTTGGGGGCGTCGCAAGGGCTCTCGCACGCTGTGAGGGTCCTTG 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide sequences from hepatitis C virus - and related vectors, polypeptide(s) and antibodies, useful for immunisation, treatment, diagnosis and typing of HCV isolates
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Best Local Similarity 99.5%; Pred. No. 4.6e-177;
Matches 599; Conservative 3; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                   Hepatitis C virus, HCV, primer, probe, detection, diagnosis, classification; immunisation; prophylaxis; serotyping; se.
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                                                                    AAQ78049 standard; cDNA; 959 BP
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                                                                                                                     Compositions comprising at least 5, and pref. 8 or more contiguous nuclectides selected from an HCV type 3 genomic sequence, more particularly (i) the region spanning positions 417-957 of the Core/El region of HCV subtype 3a; (ii) the region spanning positions 6464-4730 of the NS3 region of HCV type 3; (iii) the region spanning positions 4892-5292 of the NS3 4 region of HCV type 3; (iv) the region spanning positions 8023-8235 of the NS5 region of HCV type 3; (iv) the stop of HCV subtype 3a; or (v) an HCV subtype 3c genomic sequence, or from a subtype 2d genomic sequence, or the coding region of subtype 5a, may be used as primers to amplify nucleic acid from an isolate belonging to a specific compositions may be used for specific detection/classification of nucleic acid. Polypeptides encoded by the nucleides in such compositions may be used for immunisation against HCV and for serotyping. This sequence corresponds to the El region of HCV subtype 5a and is taken from a clone designated PC-3-8.

(Updated on 25-MAR-2003 to correct PN field.)
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                                      New polynucleotide sequences from hepatitis C virus - and related vectors, polypeptide(s) and antibodies, useful for immunisation, treatment, diagnosis and typing of HCV isolates
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                                                                                                                                                                                                                                                                                                                                                                                                                               94.8%; Score 597.2; DB 15; Length 959; 99.5%; Pred. No. 6.1e-176;
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 959 BP; 188 A; 287 C; 270 G; 214 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                             Claim 3; Page 141-142; 404pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.5
Matches 599; Conservative
WPI; 1994-358277/44.
P-PSDB; AAR63296.
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Compositions comprising at least 5, and pref. 8 or more contiguous nuclectides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning positions 417-957 of the Core/E1 region of HCV ubtype 33; (11) the region spanning positions 4892-529 of the NS3/4 region of HCV type 3; (11) the region spanning positions 8492-529 of the NS3/4 region of HCV type 3; (11) the region spanning positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype 36; (1v) the sequence, or, from a subtype 26 genomic sequence, or, from a subtype 26 genomic sequence, or the coding region of subtype 5a, may be used as primers to amplify nucleic acid from an isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid. Polypeptides encoded by the nucleotides in such detection of antibodies directed against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the E1 region of HCV subtype 5a and is taken from a clone designated PC-41.
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2..580
/*tag= a
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P-PSDB; AAR63293.
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                                                                                                                                                                                                                           compositions comprising at least 5, and pref. 8 or more contiguous nuclectides selected from an HCV type 3 genomic sequence, more nuclectides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning positions 417-957 of the core/EI region of HCV subtype 3; (1i) the region spanning positions 6023-8235 of the NS3 region of HCV type 3; (1ii) the region spanning positions 8023-8235 of the NS5 region of the BR36 sequence, or, from a subtype 2d genomic sequence, or, from a subtype 2d genomic sequence, or, from a subtype 2d genomic sequence, or the coding region of subtype 5a, may be used as primers sequence; or the coding region of subtype 5a, may be used as primers capentype, or as a probe for specific detection/classification of nucleic acid. Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the EI region of HCV subtype 5a and is taken from a clone designated PC-4-6.
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                                                                                              New polynucleotide sequences from hepatitis C virus - and relate, vectors, polypeptide(s) and antibodies, useful for immunisation, treatment, diagnosis and typing of HCV isolates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 580 BP; 111 A; 165 C; 155 G; 149 T; 0 other;
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                                                                                                                                                                                          Claim 3; Page 135-136; 404pp; English.
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Matches 580; Conservative
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Stuyver
                                        WPI; 1994-358277/44.
                                                               P-PSDB; AAR63294
Maertens G,
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                                                          GTCGCAAGGGCTCTCGCACACGGTGTGAGGGTCCTTGAGGACGGGGTAAACTATGCAACA
                                                                            61 GTCGCAAGGGCTCTCGCACACGGTGTGGTGCTTGAGGACGGGGTAAACTATCCAACA
                                                                                                                 121 GGGAATITACCCGGTTGCTCTTTCTCTTTATTCTTGCTCTTCTCTCGTGTCTGACC
                                                                                                                                                                                                                               265 TGCCCAAACTCTTCCATAGTCTATGAGGCAGATAACCTGATCCTACACGCACCTGGTTGC
                                                                                                                                                                                                                                                                                    325 GIGCCTIGIGICALGACAGGIAAIGIGAGIAGAIGCIGGGICCAAAIIACCCCIACAG
                                                                                                                                                                                                                                                                                                                                            385 TCAGCCCCGAGCCTCGGAGCAGTCACGGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCG
                                                                                                                                                                                                                                                                                                                                                            361 TCAGCCCCGAGCCTCGCAGGCAGTCACGGCTCCTTCGGAGGCCGTTGACTAGCG
                                                                                                                                                                                                                                                                                                                                                                                                    GGAGGGGCTGCCCTCTGCTCCGCGTTATACGTAGGACGCGTGTGGGGCACTATTCTTG
                      1 ACGIGCGGATICGCCGATCTCATGGGGTACATCCCGCTCGTAGGCGGCCCCGTTGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                               421 GGAGGGCTGCCCTCTGCTCCGCGTTATACGTAGGAGACGCGTGTGGGGGCACTATTCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 GTAGGCCAAATGTTCACCTATAGGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGT
     25 ACGTGCGGATTCGCCGATCTCATGGGGTATATCCCGCTCGTAGGCGGCCCCCATTGGGGGC
                                                                                                                                                                       GTTCCGGCCTCTGCAGTTCCCTACCGAAATGCCTCTGGGATTTATCATGTTACCAATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 565 TCCATTACAGTGGCCATGTTACCGGCCACCGGATGGC 602
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93EP-0402019
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(first entry)
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05-AUG-1993;
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18-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more particularly (i) the region spanning positions 417-957 of the Core/El region of HCV subtype 3a, (ii) the region spanning positions 4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning positions 8023-825 of the NS3/4 region of HCV type 3; (iv) the region spanning positions 8023-825 of the NS5 region of the BR36 subgroup of HCV subtype 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primars to amplify nucleic acid from an isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid. Polypeptides encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide sequences from hepatitis C virus - and related vectors, polypeptide(s) and antibodies, useful for immunisation, treatment, diagnosis and typing of HCV isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the El region
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                                                                                                                                                                                                                         Hepatitis C virus; HCV; primer; probe; detection; diagnosis; classification; immunisation; prophylaxis; serotyping; ss.
TTCCATTTACAGTGGCCATGTTACCGGCCACCGGATGGCA 603
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                                                                                                                                                                                                                                                                                                                                           polypeptide
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/*tag= a
/product= El p
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                                                                                                 AAQ78092 standard; cDNA; 579
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93EP-0402019
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                                                                                                                                                       (updated)
(first entry)
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05-AUG-1993;
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15-AUG-1995
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Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more nucleotides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning positions 417-957 of the Core/EI region of HCV subtype 33; (ii) the region spanning positions 8023-823 of the NS3/4 region of HCV type 3; (iii) the region spanning positions 8023-823 of the NS5 region of HCV subtype 3c genomic subgroup of HCV subtype 3d; or (v) an HCV subtype 3c genomic subgroup of HCV subtype 3d; or (v) an HCV subtype 3c genomic sequence, may be used as primers to amplify nucleic acid from a solution of a specific genotype, or as a probe for specific genotype, or as a probe for specific detection/classification of nucleic acid. Polypeptides encoded by the nucleotides in such compositions may be used for immunisation cand for section of antibodies directed against HCV and for serotyping. This sequence corresponds to the EI region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 ACGIGCGGATICGCCGAICTCATGGGGTAIATCCCGGTCGTAGGCGGCCCCAITGGGGGC
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Scone Similarity 92.6%; Pred. No. 7e-149;
36; Conservative 0; Mismatches 43; Indels 0;
                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; primer; probe; detection; diagnosis; classification; immunisation; prophylaxis; serotyping; ss.
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(Updated on 25-MAR-2003 to correct PN field.)
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1..579
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93EP-0402019.
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(first entry)
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P-PSDB; AAR63355.
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15-AUG-1995
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                                                                                                                                                                                                                                                                                                                      Compositions comprising at least 5, and pref. 8 or more contiguous nuclectides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning positions 417-957 of the particularly electron of HCV subtype 3a; (1i) the region spanning positions of HCV subtype 3a; (1i) the region spanning positions 4892-5292 of the NS3/4 region of HCV type 3; (1i) the region spanning positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to amplify nucleic acid from an sequence, may be used as primers to amplify nucleic acid from an capture belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid. Polypeptides encoded by the nucleotides in such compositions may be used for immunisation the nucleotides in such compositions may be used dor immunisation gainst HCV gainst HCV, for the detection of antibodies directed against HCV and incompositions may be used spainst HCV and incompositions may be used for immunisation of nucleotides directed against HCV and incompositions may be used for immunisation of nucleotides directed against HCV and incompositions may be used for immunisation of nucleotides directed against HCV and incompositions may be used against HCV and incompositions may be used against HCV and incompositions may be used against HCV and incompositions may be used against HCV and incompositions may be used against HCV and incompositions may be used against HCV and incompositions may be used against HCV and incompositions may be used against HCV and incompositions may be used against HCV and and incompositions may be used against HCV and and incompositions may be used against HCV and and an incompositions may be used against HCV and an incomposition of antibodies directed against HCV and an incomposition of antibodies directed against HCV and an incomposition of antibodies directed against HCV and an incomposition of antibodies directed against HCV and an incomposition
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                                                                                                                                                                                  New polynucleotide sequences from hepatitis C virus - and related vectors, polypeptide(s) and antibodies, useful for immunisation, treatment, diagnosis and typing of HCV isolates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 579 BP; 104 A; 166 C; 162 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        565 TCCATTTACAGTGGCCATGTTACCGGCCACCGGATGGCA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                    Disclosure; Page 245-246; 404pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 92.6%;
Matches 536; Conservative
                                  SA.
                               (INNO-) INNOGENETICS NV
                                                                                Maertens G, Stuyver
                                                                                                                          WPI; 1994-358277/44
                                                                                                                                                     P-PSDB; AAR63375.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GGAGCGGTCCTCTTCGGAGGGTCGTTGACTTAGCGGGAGGGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 GTTCCCTACCGAAATGCCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTCCCCTACCGAAATGCCTCTGGGGTTTATCATGTCACCAATGATTGCCCAAACTCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 ATAGICIAIGAGGCAGAIAACCIGAICCIACACGCACCIGGIIGCGIGCCIIGIGICAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 ACAGGTAATGTGAGTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGCAGTCACGGCTCCTCTTCGGAGGCCGTTGACTACCTAGCGGGAGGGCCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 TGCTCCGCGTTATACGTAGGAGACGCGTGTGGGGCACTATTCTTGGTAGGCCAAATGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           520 ACCTATAGGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     El; envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                                                                                                     AAQ83891 encodes AAR69680 hepatitis C virus (HCV) envelope 1 (E1) protein isolate SA5, both can be used for the diagnosis of HCV infection, and in the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may also be used to inhibit the expression of the HCV E1 gene.
(Updated on 25-WAR-2003 to correct PN field.)
                                             Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-nucleotide(s), peptide(s) and proteins, used in diagnosis and in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATATCACCGGCCACCGAATGGCATGGGACATGATGATGATTGGTCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGTTACCGGCCACCGGATGGCATGGGATATGATGATGAACTGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                              IndelB
                                                                                                                                                                                                                                                                                                                                                   Sequence 576 BP; 106 A; 161 C; 168 G; 141 T; 0 other;
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/product= envelope-1_protein
/note= "does not contain start or
                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 347.2; DB 10
Pred. No. 5.3e-98;
0; Mismatches 38
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1..576
/*tag= a
                                                                                                                                             Claim 1; Page 77; 186pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.7
Matches 370; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT16605 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
         P-PSDB; AAR69680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hepatitis; ss
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AAT16605
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GTCGCAAGGGCTCTCGCACACGGTGTGAGGGTCCTTGAGGACGGGGGTAAACTATGCAACA
                                                                                                                                                                                                                                                                                                   181 GICCCGGCCTCTGCAGITCCCTACCGAATGCCTCTGGGATCTATCATGTCACCAATGAT
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diagnosis; vaccines; antibodies; antisera; gene inhibition; ss.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                             ATAGICIAIGAGGCAGAIAACCIGAICCIACACGCACCIGGIIGCGIGCCIIGIGICAIG 339
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                                                                                                                                                                                              AAT16559-T16609 are CDNAB encoding the El (envelope-1) protein of 51 H isolates. The isolated sequences are useful for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccinse for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of HCV infection.
                                                                                                                                                                                                                                                                                                                                                       220 GITCCTACCGAAATGCCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCC
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                                                                                                                                            DNA and amino acid sequence of HCV envelope 1 and core proteins -
used to determine HCV genotype and as vaccines against HCV infection
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                                                                                                                                                                                                                                                                                                             55.1%; Score 347.2; DB 17; Length 576; 90.7%; Pred. No. 5.3e-98; ive 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGITACCGGCCACCGGATGGCATGGGATATGATGATGATGTAA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 576 BP; 106 A; 161 C; 168 G; 141 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus envelope 1 gene cDNA isolate SA7.
                                                                 DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                               Claim 1; Page 107; 340pp; English
                                                                                              Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ83893 standard, cDNA; 576
                         95WO-US10398
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(first entry)
                                             94US-0290665
                                                                 (USSH ) US DEPT HEALTH & HI
(USSH ) US SEC DEPT HEALTH.
                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 90.7
Matches 370; Conservative
                                                                                                Miller RH,
                                                                                                                    WPI; 1996-139709/14
                                                                                                                               P-PSDB; AAR89551
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(Updated on 25-MAR-2003 to correct PN field.)
Hepatitis C virus, HCV; non-A non-B; envelope 1 gene; isolate SA7; diagnosis, vaccines; antibodies; antisera; gene inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-nucleotide(s), peptide(s) and proteins, used in diagnosis
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54.6%; Score 344; DB 16; Length 576;
Best Local Similarity 90.2%; Pred. No. 5.3e-97;
Matches 368; Conservative 0; Mismatches 40; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 CATGTTACCGGCCACCGGATGGCATGGATGATGATGATGAACTGGTAA
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                                                                                                                      Location/Qualifiers
1..576
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                                                                                 Hepatitis C virus.
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280 ATAGTCTATGAGGCAGATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCTCTG 339
                                241 TGCTCCGCGCTATACGTCGGGGACGCGTGCGGGGCAGTGTTTTTGGTAGGCCAGATGTTC
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    460 TGCTCCGCGTTATACGTAGGACGCGTGTGGGGGCACTATTCTTGGTAGGCCAAATGTTC
                                                                                    520 ACCIAIAGGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus, HCV, non-A non-B; envelope 1 gene; isolate SA6; diagnosis, vaccines; antibodies; antisera; gene inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ83892 encodes AAR69681 hepatitis C virus (HCV) envelope 1 (E1) protein isolate SA6, both can be used for the diagnosis of HCV infection, and in the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may also be used to inhibit the expression of the HCV E1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived
oligo-nucleotide(s), peptide(s) and proteins, used in diagnosis
and in vaccines
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                                                                                                                                                                                            361 CATATCACCGGCCACCGAATGGCATGGGACATGATGATGATTGGTCA 408
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                                                                                                                                                                                                         envelope 1; core protein; HCV genotyping; antibody; vaccine;
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/note= "does not contain start or stop codon"
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Pred. No. 5.3e-97;
0; Mismatches 40; Indels
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                                                                                                                                                              Hepatitis C virus isolate SA7 envelope 1 gene
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(USSH ) US SEC DEPT HEALTH.
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Best Local Similarity 90.2%;
Matches 368; Conservative (
                                         AAT16607 standard; cDNA; 576
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RESULT 14
                 AAT16607
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Db 61 ATAGTCTATGAGGCTGATGACCTGACCTGACCTGGCTGCGTGCCCGG 120

Qy 340 ACAGGTAATGTGAGGTCCAAATTACCCCTACACTGTCGGCCCGAGCCTC 399

121 AAGGATAATGTCAGTACATGCTGGATCCATATCACCCCTACACTGCCGGAGCCTC 399

400 GGAGCAGTCACGGCTCCTCTTCGGAGAGCCGTTGACTACCACTATCAGCCCGAGCCTC 459

400 GGAGCAGTCACGGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCGGAGGCCCCCTC 459

181 GGAGCGGTCACGGCTCCTCTTCGGAGAGCCGTTGATTACTTGGTAGGCCGCCTC 240

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Search completed: December 19, 2003, 18:51:24 Job time : 175.169 secs

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Eukaryotes, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases I to 488)

2 Zabo, M., Huang, Q., Xu, X., Li, Y., Seng, Y., Song, H., Xiao, H., Cu, Y., Li, N., Qian, B., Liu, P., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, J., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gao, G., Wang, Z., Zhang, Q., Chen, S., Han, Z. and Chen, Z. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zeguang Han
Contact: Zeguang Han
Contact Human Genome Center at Shanghai
State Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Part: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Fax: 86-21-50801922
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AV755731
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This clone is available at CHGC in Shanghai
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Database

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us-09-899-303a-31.rst

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University Submission

Submitted (102-1014-1999) Genoscope - Centre National de Sequencage :

By 191 191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila melanogaster ganome using these BACs. For further information and manoser in Pieter de Jong's laboratory in the Department of Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Scognic strain y2; cn bw sp, the same strain used for the BDGP's isogenic strain y2; cn bw sp, the same strain used for the BDGP's Illerary and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                        920 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR13J24 of RPCI-98 library from Drosophila melanogaster (fruit AL061710
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CTCTGCTCCGCGTTATACGTAGGACGCGTGTGGGGCACTATTCTTGGTAGGCCAAATG
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Best Local Similarity 18.0%; Pred. No. 15;
Matches 55; Conservative 124; Mismatches 126;
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi,
I (bases I to 492)
I (bases I to 492)
Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,
Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng
J., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G.,
Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z.
Unpublished
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
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Best Local Similarity 66.3%; Pred. No. 9.4e-05;
Matches 114; Conservative 0; Mismatches 54; Indels
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This clone is available at CHGC in Shanghai.
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/clone="CSCCAPO04YJ09"
/tissue_type="THYMUS"
/clone llb="Homo sapiens THYMUS"
/note="Vector: pcMVSPORT_6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
                                                                                                                              BX437004 BX 944 bp mRNA linear BST 15-MAY-2003 BX437004 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP004YJ09
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BX443048 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA clone CS0DG003Y007 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedax - France
BMail: Sequef@genoscope.cns.fr, Webno.de.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6927.f For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSoCAP004CE05NP1&cluster=6927.f. Contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 GTGAGGGTCCTTGAGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 GMGGGKGMMKGGAMGGGMKMNVTTGTMTWTTGAMMGGTGMMTGTMMTTGTHTTTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 TCTATCTTTATTCTTGCTCTTCTCTCGTGTCTGACCGTTCCGGCCTCTGCAGTTCCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 CGAAATGCCTCTGGGATTTATCATGTTACCAATG-ATTGCCCAAACTCTTCCATAGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CS0CAP004CE05NP1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
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       612 TTTTCAATTTTTTTMAAWATTYMC 588
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BX437004
                                                                                                                                                                                                                                BX437004.1 GI:30771523
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Mammalia; Eutheria;
1 (bases 1 to 944)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cadex - France
BP 191 91006 ENRY cadex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3822.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODB008DA06QPl&cluster=3822.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODB008DA06QPl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX374637
BX374637 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens CDNA clone CSODB008YB12 5-PRIME, mRNA sequence.
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596 YBYBYAAYKASYBYKTSBKKCKSTCKSCSTBMTCSYDCYBVYBCYCYAYCKBYYCCCYBY 655
                                                                                                                                                                             TGTCATGACAGGTAATGTGAGTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCC 392
                                                                                                                                                                                                         /tissue type="NEUROBIASTOMA COT 10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBIASTOMA COT 10-NORMALIZED"
/clone="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Pive prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

151 c 243 g 205 t 156 others
                                                                          CTCTTCCATAGTCTATGAGGCAGATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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41.4%; Pred. No. 22;
tive 25; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="CS0DB008YB12"
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8 셤 ò 엄 8 us-09-899-303a-31.rst

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BI462364 1721 bp mRNA linear EST 21-AUG-2001
603203722F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5269756 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="148-3008"
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/tissue_type="Leaf, 48 h 0.4M NaCl"
/clone_lib="Six week old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library
/ 48 hours NaCl treatment"
/ 48 hours NaCl treatment"
/ Flooris Site 2: Xhol"
/ Inote="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_l:
/ Iso c 1.78 g 205 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 721)

NIH-WGC http://mgc.nci.nih.gov/.

NIH-WGC http://mgc.nci.nih.gov/.

Unpublished

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 GTCGCAAGGGCTCTCGCACACGCTGTGAGGTCCTTGAGGACGGGTAAACTATGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    529 dradsakarddarticaccrcdrantakrdardarddaddadddaddaddaraddradd
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                      plant
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Best Local Similarity 51.5%; Pred. No. 43;
Matches 84; Conservative 0; Mismatches 79; Indels 0;
                                                                                                    An expressed sequence tag database for the common ice Mesembryanthemum crystallinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 GITCCGGCCTCTGCAGITCCCTACCGAAATGCCTCTGGGATIT 247
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/organism="Mesembryanthemum crystallinum"
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                                                                                                                                                                                            Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Fax: 775-784-1918
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High quality sequence stop: 350
POLYA=No.
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/db_xref="taxon:3544"
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                                                                                                                                                                                                                                                                                                                            Email: jcushman@unr.edu
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Cushman, J.C.
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//organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
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/tissue type="B CELLS (RAMOS CELL LINE)"
/clone="type="B CELLS (RAMOS CELL LINE)"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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Mesembryanthemum crystallinum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                         Eukaryorta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1201)
Li, Wa B., Gruber, C., Jessee, J. and Polayes, D. Full.length, cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                 Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 FVRX cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3085.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODG003AH04QP1&cluster=3085.r. Contact
cgi-bin/cluster.cgi?seq=CSODG003AH04QP1&cluster=3085.r. Contact
Feng Liang Email : fliang@lifetch.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODG003AH04QP1.
Location/Qualifiers
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5.9%; Score 37; DB 13; Length 12
Best Local Similarity 41.1%; Pred. No. 37;
Matches 90; Conservative 21; Mismatches 108; Indels
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184 c 261 g 350 t
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                                         BX443048
BX443048.1 GI:31018553
                                                                                                         Homo sapiens (human)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/db one="CSODIO15YBO3"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo gapiens PLACENTA COT 25-NORMALIZED"
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BP 191 91006 EVRY cedex - France
Email: sequenceGenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com U
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence.ID : CSODIO15CAO2NP1.
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                                                                                                                                                                                                                                                                            Length 962;
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                                              /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="texon:7227"
/db_xref="texon:7227"
/clone="BACN12J12"
/clone=lib="DrosBAC"
/plasmid="pBeloBAC11"
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                                                                                                                                                                                                                                                                          DB 29;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution. information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11680 row: k column: 05
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 962)
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High quality sequence stop: 712.
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55.0%; Pred. No. 44;
iive 0; Mismatches
                                                                                                                                                                                                                       /organism="Homo sapiens".
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/clone="IMAGE:5269756"
/lab_host="DH108"
/clone_lib="NIH_MGC_97"
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BX384351
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCMYSPORT 6 vector. Library was normalized." 88 c 93 g 398 t 506 others
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/mol type="mtkl taxon:966"
/db Xref="taxon:966"
/clone="CSODKOOBYD04"
/cell type="HELA CELLS COT 25-NORMALIZED"
/cell line="HELA"
/cell line="HELA"
                                                                                                                                                                                                  155 CCGGTTGCTCTTTCTTTATTCTTGCTCTTCTCTCGTGTCTGACCGTTCCGGCCT
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                                                                                                                                                                                                                                                                                             Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Bmail: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2147.f
more information about this cluster, see
http://www.genoscope.cns.fr,
                                                                                                                                                                   Сарв
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                                                                                                                               Length 1201;
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1 Similarity 15.3%; Pred. No. 53;
48; Conservative 133; Mismatches 133;
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 405)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins Chissoe, S., Dietrich, N., Dacy, M., Le, M., Le, N., Mardis, B., Moore, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, B., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fex: 314 286 1810
Email: estGwatson.wustl.edu
This clone is available royalty-free through LINL; contact the
This clone is available royalty-free through LINL; contact the
This clone is available royalty-free through LINL; schraution.
INAGE Consortium (infe@dimage.llnl.gov) for further information.
INAGE Length: 1873 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 391.
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCNVSPORT 6 vector. Library was normalized." 252 c 194 g 261 t 131 others
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ze65a12.r1 Soares retina N2b4HR Homo sapiens CDNA clone IMAGE:363838 5', mRNA sequence.
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                                                                                                                                                                                                            5.7%; Score 35.8; DB 13; Length 918; 36.0%; Pred. No. 74;
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/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                             93;
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35; Mismatches
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/db_xref="GDB:1280541"
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/clone="IMAGE:363838"
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BG571230 962 bp mRNA linear EST 10-APR-2001
602592170F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4719520 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.l column: 17
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="NIH MGC_79"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 AACAGGAATTTACCCGGTTGCTCTTTCTCTTTATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 AATGGGGANGGCTGGGCCGGCTGTCTCTCAACGACTGTT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35.4; I
Pred. No. 83;
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High quality sequence stop: 180.
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BX397483 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI036YA06 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 13-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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BP 191 91006 EVRY cedex - France
BF 191 91006 EVRY cedex - France
BFMail: seqrefégenoscope.cns.fr was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 434.f For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

118 c 175 g 236 t 382 others
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1178)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genoscope.cns.fr/
gl-bin/Cluster.cgi?seg=CS0D1036BA03QPl&cluster=434.f. Contact :
Fag-bin/Cluster.cgi?seg=CS0D1036BA03QPl&cluster=434.f. Contact :
Feng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1036BA03QPl.
Location/Qualifiers
1. 1178
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Pred. No. 96;
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/note="Vector: pBluescript II KS(+); Site_1: ECORI;
/note="Vector: pBluescript II KS(+); Site_1: ECORI;
/note="Vector: pBluescript II KS(+); Site_1: ECORI;
/note="Vector: primer, using methylated from initiated using an oligo day primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, lighted to NotI and ECORI compatible sites of a closed modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Aves; Chordata; Craniata; Vertebrata; Euteleostomi; Butchosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 727)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simon Hubbard
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                           BU425620
603961926F1 CSEQREN09 Gallus gallus cDNA clone ChEST938d8 5', mRNA
167 TCTCTATCTTTATCTTTGCTCTTCTCGTGTCTGACCGTTCCGGCCTCTGCAGTTCCCT 226
1044 TKACKTKCTBKKKBAKMTKKCTKMKBACAMATKKMBMTKKKTKKTCCCTKNTBACCMTK 985
                                                                                                   286
                                                                                                                             984 BMCCCYKKKCCKCWMHCYCMTKTTMCCTTMMTGTKTTMCMYMCGTTTYTTCYKCMKUCCMT 925
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|sex="Male and female"
|/issue_type="Chondrocytes isolated from growth plate
                                                                                                227 ACCGAAATGCCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCT
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
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5.6%; Score 35.2; DB 13; Length 727;

Query Match

Search completed: December 20, 2003, 06:55:03 Job time : 1628.71.8ecs

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 December 19, 2003, 18:11:23 ; Search time 45.4354 Seconds (without alignments) 6120.154 Million cell updates/sec
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1 ATGGTAAGGTCATCGATAC......TGATGATGAACTGGTAATAG 630
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
               5.1.6
Compugen Ltd.
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PCT-US95-10398-50
                                                                                                                                                                                                                                                                                   569978 seqs, 220691566 residues
                GenCore version (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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US-08-08-428B-45
US-08-08-570-45
US-08-46-601A-45
PCT-US95-10398-45
US-08-470-426B-17
US-08-470-426B-17
US-08-612-973-5
US-08-612-973-5
US-08-927-597-47
US-08-927-597-47
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US-08-927-597-47
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US-08-927-597-47
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US-08-927-597-47
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ALIGNMENTS

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APPLICANT: MARKTENS, GERRT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARTYNOFF,
APPLICANT: BUYSE, MARTYNOFF,
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: RC-DUS/MS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
FILING DATE: 11-MAR-1996
GLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 1487-10
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: 1 linear
                                                                                                                                                                                                                                                                                                                                            STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 31, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
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us-09-899-303a-31.rni

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241 GGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCAGATAAC 300
241 GGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCAGATAAC 300
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 3.4e-192;
Matches 630; Conservative 0; Mismatches 0;
                                                          PRIDACATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS 32,205
REFERENCE/DOCKET NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUICATION INFORMATION:
TELECHOMICATION INFORMATION:
TELECHOMICATION INFORMATION:
TELECHOMO TELECHOMO
TELECHOMO FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
"VPOTHETICAL: NO
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ANTI-SENSE: NO
FEATURE:
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FEATURE:
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Sequence 31, Application US/08927597

Sequence 31, Application US/08927597

Sequence 31, Application US/08927597

GENERAL INFORMATION:
APPLICANT: BOSMAN, FONS

APPLICANT: BOSMAN, FONS

TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STREET: 10.5.A.

ZIP: 22201-4714

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE
                                                                                                                           1 ATGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTAATATCCCG
                                                                                                                                                                                                                                                                                                                      1 ATGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTATATCCCG
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                                                                           Gaps
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0
                                              Length 630;
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                                             Query Match 100.0%; Score 630; DB 3; I Best Local Similarity 100.0%; Pred. No. 3.4e-192; Matches 630; Conservative 0; Mismatches 0;
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                    US-08-612-973-31
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  400 GGAGCAGTCACGGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCGGGAGGGGCTGCCCTC
                                            181 GGAGCGGTCACGGCTCCTCTTCGGAGGGTCGTTGACTTTAGCGGGAGGGGCTGCCCTC
                                                                                                                                                                               520 ACCTATAGGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGC
                                                                                         460 TGCTCCGCGTTATACGTAGGAGACGCGTGTGGGGCCACTATTCTTGGTAGGCCAAATGTTC
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED PROW THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
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Pred. No. 1.5e-101
0; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGRUT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47, Application US/08468570 Patent No. 5871962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.7%;
Matches 370; Conservative
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US-08-468-570-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BUKH, J., MIL
APPLICANT: PURCELL, R.H.
TITLE OP INVENTION: ANIN
TITLE OF INVENTION: OF 5
TITLE OF INVENTION: OF 7
TITLE OF INVENTION: OF 7
TITLE OF INVENTION: DIAG
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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NEW YORK
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GCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGCCATGTTACCGGCCACGGATG 600
                                            541 GCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGCCATGTTACCGGCCACCGGATG 600
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NUCLECTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
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Pred. No. 1.5e-101;
0; Mismatches 38;
                                                                                         630
                                                                                                                601 GCATGGGATATGATGAACTGGTAATAG 630
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,428B
FILING DATE: 29-UNN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFRAK: (212) 751-6849
                                                                                                                                                                                                                                        Sequence 47, Application US/08086428B Patent No. 5514539 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MORGAN & FINNEGAN
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TELEY 421792
TELEY A 1792
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.1%;
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INDIVIDUAL ISOLATE: SAS
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Best Local Similarity 90.7
Matches 370; Conservative
                                                                                                                                                                                                                                                                                                         APPLICANT: BUKH, J., MIL
APPLICANT: PURCELL, R. H.
TITLE OF INVENTION: ANIN
TITLE OF INVENTION: OF 5
TITLE OF INVENTION: OF 7
TITLE OF INVENTION: OF 7
TITLE OF INVENTION: DIAGNORER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NEW YORK
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US-08-086-428B-47
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APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE I GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERLYDE PROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOKANA & FINNEGAN
STREET: 345 PARK AVENUE
CITYLE OF WALL OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE 
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                                                                                                 Length 576;
                                                                                                                                                   Indels
                                                                                                                                                      38;
                                                                                                 DB 2;
                                                                                           Score 347.2; DB 2;
Pred. No. 1.5e-101;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER KEALDE FORME
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,601A
FILING DATE: 06-UJW-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-UJW-1993
CLASSIFICATION: 435
ATTORNEY/AGBAT INFORMATION:
NAME: RIGHARD W: BORK
REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 47, Application US/08466601A Patent No. 6572864
                                                                                                    55.1%;
ilarity 90.7%;
Conservative
ORGANISM: homosapiens;
INDIVIDUAL ISOLATE: SA5
US-08-290-665A-47
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COMPUTER READABLE FORM:
                                                                                                                             Similarity
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ZIP: 1019
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Best Local 8
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Matches
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Sequence 47, Application US/08290665A
Sequence 47, Application US/08290665A
GENERAL INFORMATION:
APPLICANT: BUCKH, J., MILLER, R.H. AND
APPLICANT: PUNCELL, R.H.
APPLICANT: PUNCELL, R.H.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HERAITITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: AND THE USE OF REAGENTS OF BEATITIES C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS OF REAGENTS
SEQUENCES: 263
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: FLOPEY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION 1435
ATTORNAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 30,459
REGISTRATION NUMBER: 2026-4116
TELEPHONE: (212) 759-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAN. (212) 758-4800
TELEFAN. (212) 751-6849
TELEX. 421'92
INPORMATION FOR SEQ ID NO: 47
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-290-665A-47
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NUCLECTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                           Score 347.2; DB 4;
Pred. No. 1.5e-101;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
PCT-US95-10398-47
FCT-US95-10398-47
Sequence 47, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H. AND APPLICANT: PURCELL, R.H. AND ATITLE OF INVENTION: AND THE USE OF ISCURY: TITLE OF INVENTION: AND THE USE OF ISCURY: TITLE OF INVENTION: AND THE USE OF REAG!
TITLE OF INVENTION: SEQUENCES IN DIAGNO NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
COUNTRY: USA
REFERENCE/DOCKET NUMBER: 2026-4070US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
               TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                           55.1%;
90.7%;
                                                                   TELEX: 421792
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                ORGANISM: homosapiens
INDIVIDUAL ISOLATE: SAS
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.7
Matches 370; Conservative
                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                       US-08-466-601A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520
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61 ATAGICTACGAGGCIGATAACCIGATICIGCACGCACCIGGITGCGIGCCIGIGIGIAGA 120
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Patent No. 5514539
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO AF 11 SOLATES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HERPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
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Pred. No. 1.5e-101;
0; Mismatches 38;
JMBER: PCT/US95/10398
15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
                              FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 UNB 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.7%;
Matches 370; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CT-US95-10398-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MILLER, R.H. AND
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 90.2
Matches 368; Conservative
     GENERAL INFORMATION:
APPLICANT: BUCH, J., MILL
APPLICANT: BURCELL, R.H.
TITLE OF INVENTION: NUCLE
TITLE OF INVENTION: OF 51
TITLE OF INVENTION: OF 51
TITLE OF INVENTION: OF 81
TITLE OF INVENTION: OF 81
TITLE OF INVENTION: DIAG;
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FIL
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                 10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520 ACCIATAGGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTTCCATTTACAGTGGC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AGCTATAGGCCTCGCCACACACACACGGTGCAGGACTGCAACTGTTCCATTTACAGTGGC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 344; DB 1; Length 576;
Pred. No. 1.5e-100;
0; Mismatches 40; Indels
DIAGNOSTIC METHODS AND VACCINES 159
                                                                                                                                  ZUDINITE: UD154

COMPUTER READABLE FORM:
MBDIUM TYPE: PLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,428B
FILING DATE: 29-UNN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 2026-4070
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETA: 421792
INPORMATION FOR SEQ ID NO: 49:
SEQUIENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TITLE OF INVENTION: DIAGNOSTIC NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 54.6%;
Best Local Similarity 90.2%;
Matches 368; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: homosapiens;
INDIVIDUAL ISOLATE: SA7
US-08-086-428B-49
                                                                 STATE: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: lin
ORIGINAL SOURCE:
                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400
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; Sequence 49, Application US/08468570

RESULT 9 US-08-468-570-49

61 ATAGTCTATGAGGCTGACGTGATCCTGCACGCACCTGGTTGCGTGCCTGTGTGTAGA 120 340 ACAGGTAATGTGAGTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCTC 399 180 459 240 280 ATAGICIAIGAGGCAGAIAACCIGAICCIACACGCACCIGGIIGCGIGCCIIGIGIGIAIG 339 9 220 GITCCCTACGAAATGCCTCTGGGAITTATCATGITACCAATGATGCCCAAACTCTTCC 1 GICCCCTACCGAAATGCCTCCGGGGTTTATCATGATGATGATTGCCCGAACTTCC 121 CAAAATAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACATTGTCAGCCCCGAACCTC ggagcagrcacqecrccrcrrrcggagagcgrrgacraccragcgggaggggcrccrc 460 IGCTCCGCGTIATACGIAGGAGACGCGTGTGGGGCACTATTCTTGGTAGGCCAAAIGTTC NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES 0; Length 576; Indels 54.6%; Score 344; DB 2; I 90.2%; Pred. No. 1.5e-100; iive 0; Mismatches 40; 2026-4070US1 MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERRECT 5.1
CURRENT APPLICATION UNBER: US/08/468,570
APPLICATION UNBER: US/08/468,570
FILING DATE: 6-UIN-1995
CLASSIFICATION: 424
PR.OR. APPLICATION UNBER: 08/086,428
FILING DATE: 29-UIN-1993
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REPERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849 ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK STATE: NEW YORK

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301 AGCTATAGGCCTCGCCAGCACTACGGTGCAGACTGCAACTGTTCCATTTACAGTGGC 360
                                    400 GGAGCAGTCACGGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCGGGGAGGGGCTGCCCTC
                                                                                                                                                                   241 recrececeraraceresesacecerecesesererrrresrasses de recreares de construccion de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcción de construcci
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF SI ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
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Pred. No. 1.5e-100;
0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2026-4070US2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application US/08466601A
Patent No. 6572864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      & FINNEGAN
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CITY: NEW YORK
STATE: NEW YORK
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Best Local Similarity 90.2
Matches 368; Conservative
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TITLE OF INVENTION: AMIN
TITLE OF INVENTION: OF F
TITLE OF INVENTION: OF INVENTION: OF INVENTION: OF INVENTION: DIAM
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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APPLICANT: BUKH, J.,
APPLICANT: PURCELL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MORGAN
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
263
                                                                                                                                           361 CATATCACCGGCCACCGAATGGCATGGGACATGATGATTGGTCA 408
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Pred. No. 1.5e-100;
0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPRY DISK
COMPUTER: IBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                   MILLER, R.H. AND
                                                                                                                                                                                                                                              RESULT 10
US-08-290-665A-49
'Sequence 49', Application US/08290665A
'Patent No. 5882852
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: BURGH, J., MILLER, R.H.
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: WUCLEOTIDE AP
TITLE OF INVENTION: AMINO ACID SE
TITLE OF INVENTION: CORE GENES OF
TITLE OF INVENTION: SEQUENCES IN
NUMBER OF SEQUENCES: 263
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 54.6%;
al Similarity 90.2%;
368; Conservative
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INPORMATION POR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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NEW YORK
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INDIVIDUAL ISOLATE: SA7
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Best Local Similarity
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Sequence 49, Application US/08086428B
Settle No. 5514539
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HERATITIS C AND THE USE
TITLE OF INVENTION: OF RAGENTS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                    40; Indels
                                                                                                                                                                           Score 344; DB 5; 1
Pred. No. 1.5e-100;
0; Mismatches 40;
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COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,428B
FILING DATE: 29-JUN-1993
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FINNEGAN
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IBM PC COMPATIBLE
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ACTT: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USP
ZIP: 1
                                                                                                                                                                               54.6%;
milarity 90.2%;
Conservative 0
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDENDESS: single
TOPOLLGY: linear
ORIGINAL SOURCE:
                                                                                                    ORGANISM: homosapiens
INDIVIDUAL ISOLATE: SA7
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TITLE OF INVENTION: OF S
TITLE OF INVENTION: OF S
TITLE OF INVENTION: OF R
TITLE OF INVENTION: DIAG
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: FLOPPY
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Matches 368;
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                                                                                                            61 ATAGTCTATGAGGCTGACAGACTGATCCTGCACGCACCTGGTTGCGTGCCTGTGTCAGA 120
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POT-1895-10198-49

Sequence 49, Application PC/TUS9510398

GENERAL INFORMATION:

APPLICANT: BUCKH, J., MILLER, R.H. AND

APPLICANT: PURCELL, R.H.

TITLE OF INVENTION: ANIO SEQUENCES OF THE ENVELOPE 1 AND

TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE

TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

TITLE OF INVENTION: SEQUENCES: 263

CORRESPONDENCE ADDRESS:

ADDRESSED: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STREET: MAY ORK
                             1 GTCCCCTACCGAAATGCCTCCGGGGTTTATCATGTCACCAATGATGGTTGCCCGAACTCTTCC
                                                                                                                                                                       340 ACAGGTAATGTGAGTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTC
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
RESISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECHARC (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: PLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

COMPUTER: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10398

FILING DATE: 15-AUG-1995
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TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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280 ATAGTCTATGAGGCAGATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCATG 339
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 340.8; DB 2
Pred. No. 1.6e-99;
0; Mismatches 42
                                                                                   FILING DATE: 6-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070US1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MILLER, R.H. AND
           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
APPLICATION NUMBER: 05/08/468,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 48, Application US/08290665A
Fatent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AN
TITLE OF INVENTION: NUCLEOTIDE AND I
TITLE-OF INVENTION: CORE GENES OF IS
TITLE-OF INVENTION: AMINO ACID SEQUE
TITLE-OF INVENTION: AND THE USE OF IS
TITLE OF INVENTION: AND THE USE OF IS
    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 89.7%;
Matches 366; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: homosapiens
INDIVIDUAL ISOLATE: SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: lir
ORIGINAL SOURCE:
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US-08-290-665A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
TELEX: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 GTTCCCTACCGAAATGCCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCC 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCTCCGCGTTATACGTAGGAGACGCGTGTGGGCCACTATTCTTGGTAGGCCAAATGTTC 519
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ANINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
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Pred. No. 1.6e-99;
0; Mismatches 42; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGTTACCGGCCACCGGATGGCATGGGATATGATGATGAACTGGTAA 627
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APPLICANT: PURCELL, N.H.
TITLE OF INVENTION: AMINO ACID SEQUEN
TITLE OF INVENTION: AMINO ACID SEQUEN
TITLE OF INVENTION: OF 51 ISOLATES OF
TITLE OF INVENTION: OF RAGENYE DERIVITLE OF INVENTION: DIAGNOSTIC METHODI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 48, Application US/08468570
; Patent No. 5871962
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
REFERENCE/DOCKET NUMBER: 20:
                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 54.1%;
Best Local Similarity 89.7%;
Matches 366; Conservative
                                                                                                              TELEX: 421792
INPORMATION POR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                               ORGANISM: homosapiens
INDIVIDUAL ISOLATE: SA6
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345 PARK AVENUE
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CORRESPONDENCE ADDRESS:
  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEW YORK
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US-08-468-570-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ATAGTCTATGAGGCTGATGACCTGATCCTACACGCACCTGGCTGCGTGCCTGTGTCCCGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: USA
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.1%; Score 340.8; DB 2; Length 576; Best Local Similarity 89.7%; Pred. No. 1.6e-99; Matches 366; Conservative 0; Mismatches 42; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYRE: 10154
COMPUTER: FLOPEY DISK
COMPUTER: ELOPEY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERREET 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION NUMBER: US/08/290,665A
ATTORNEY/AGENT INFORMATION:
RAFELSTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECPHONE: (212) 756-4890
TELECPHONE: (212) 756-4890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) /51-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNES: single
TOPOLOGY: linear
ORGANISM: homosapiens
INDIVIDUAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: SA6
US-08-290-665A-48
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Search completed: December 20, 2003, 07:03:17 Job time : 46.4354 secs